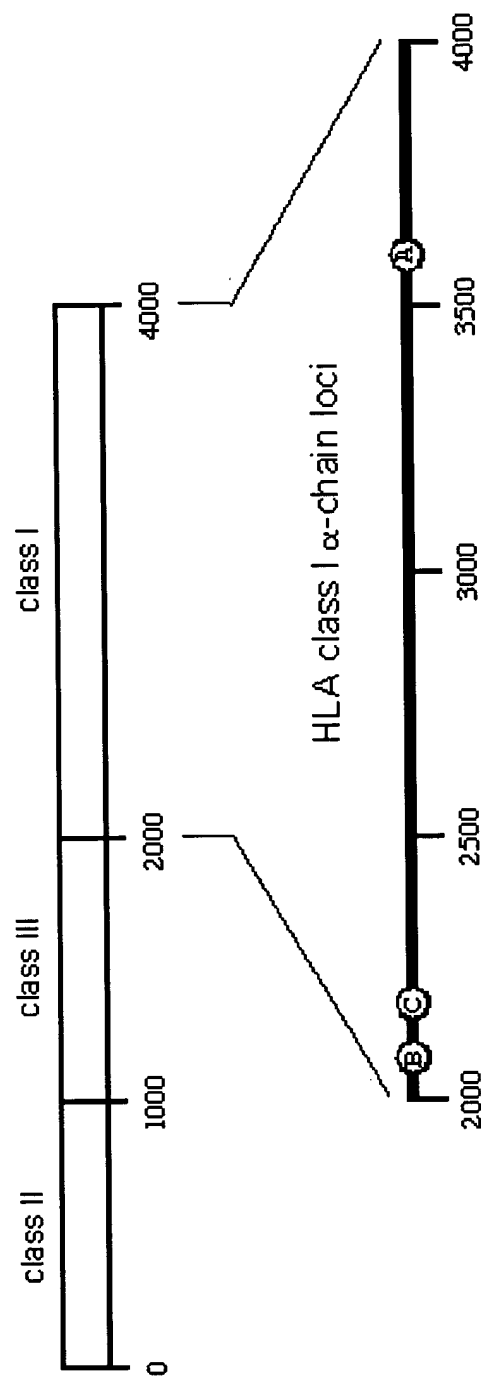


A



B

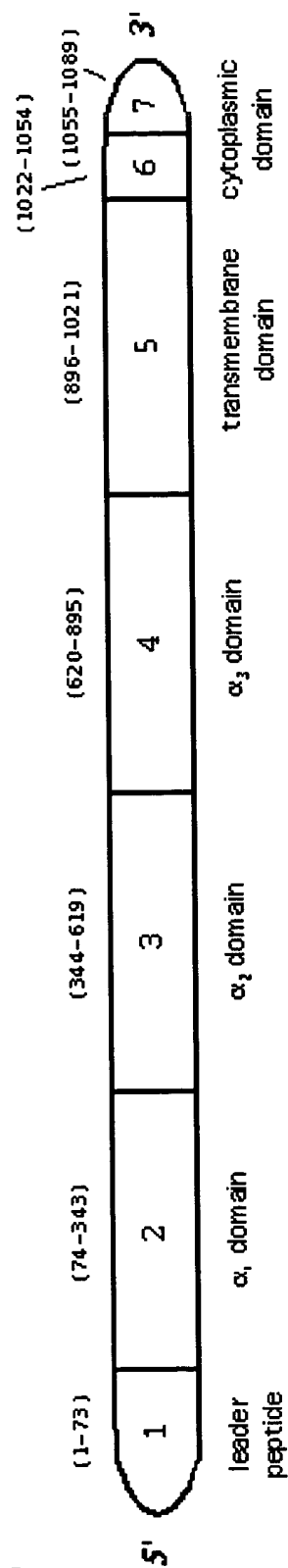


FIG. 1

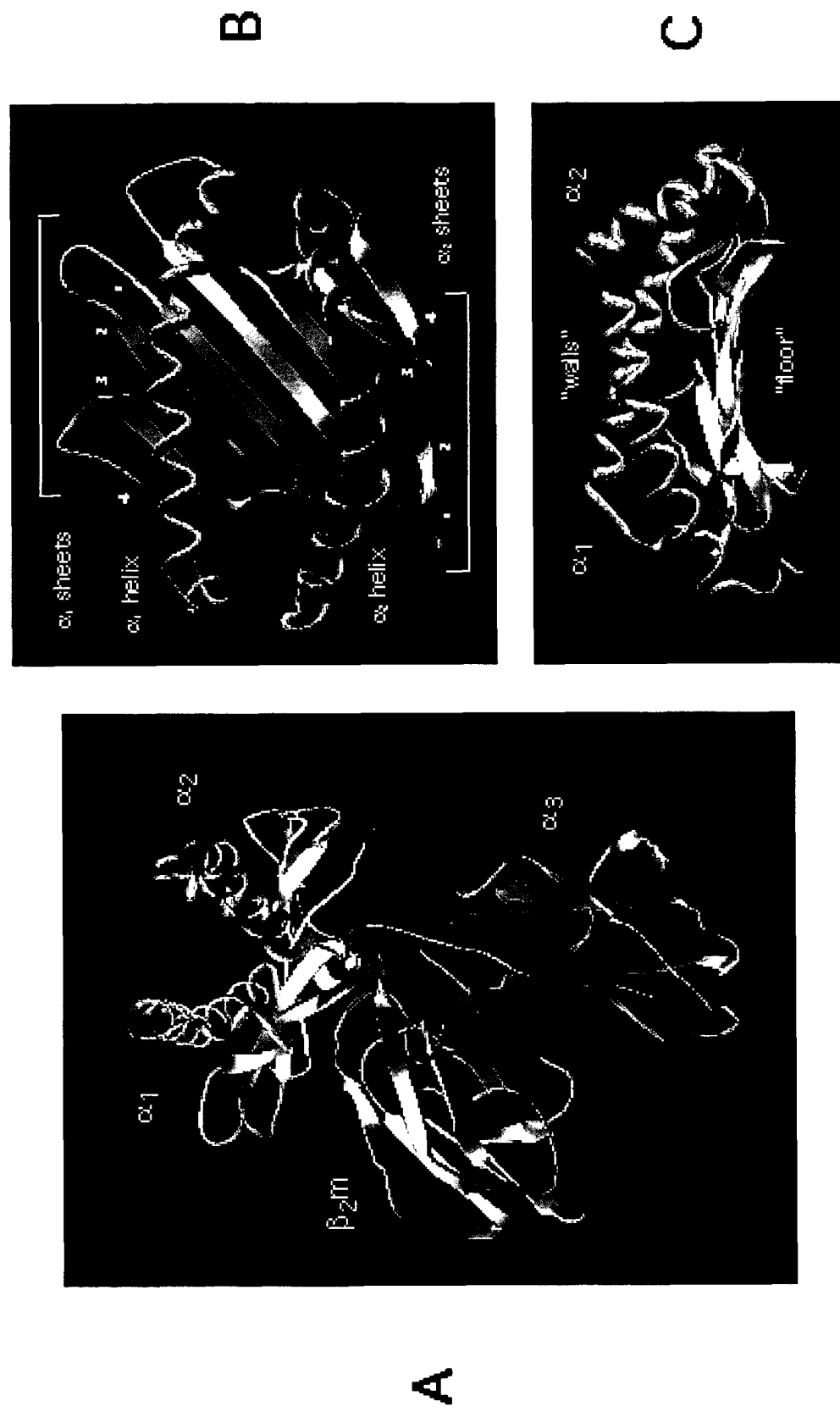


FIG. 2

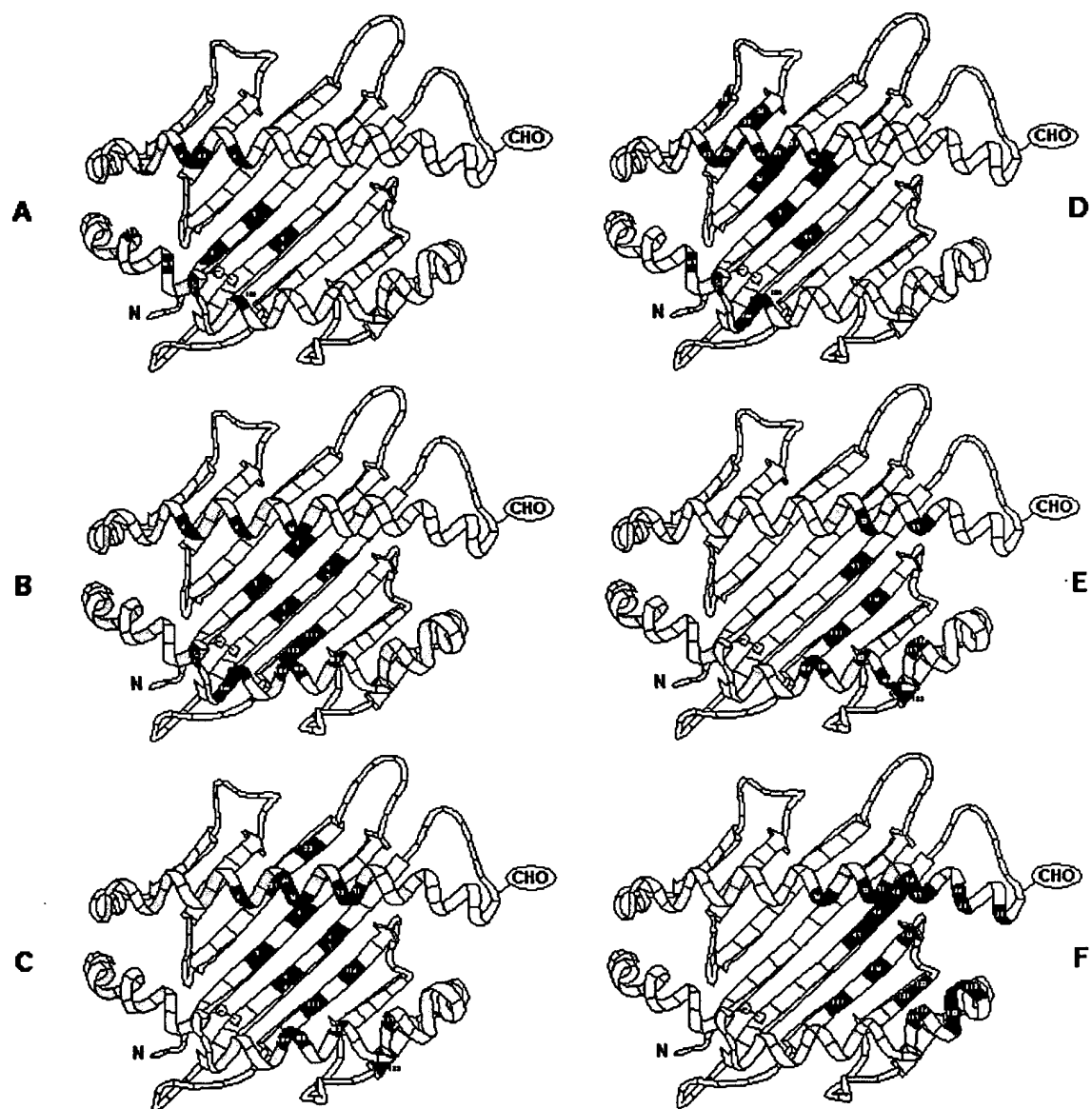


FIG. 3

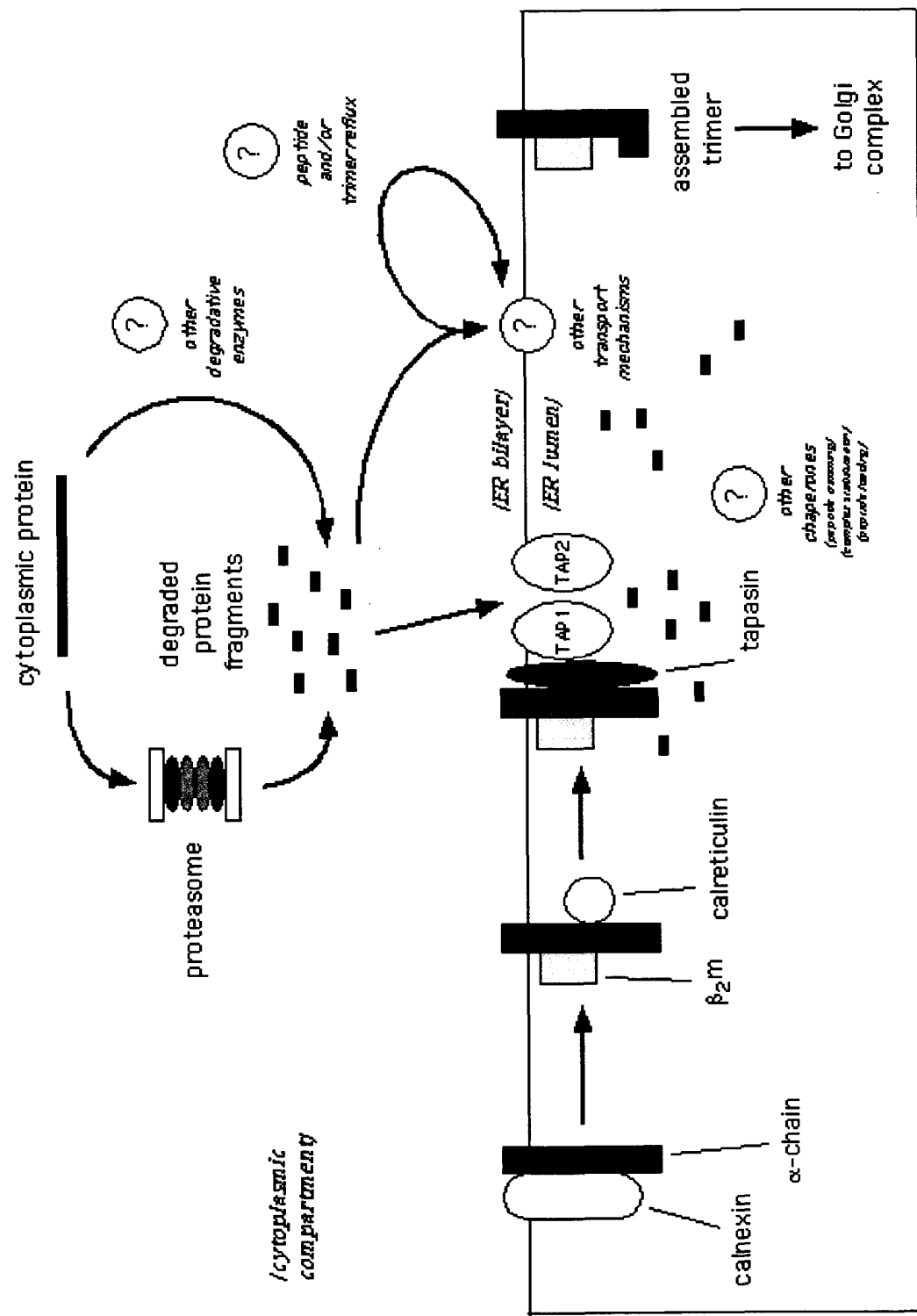


FIG. 4

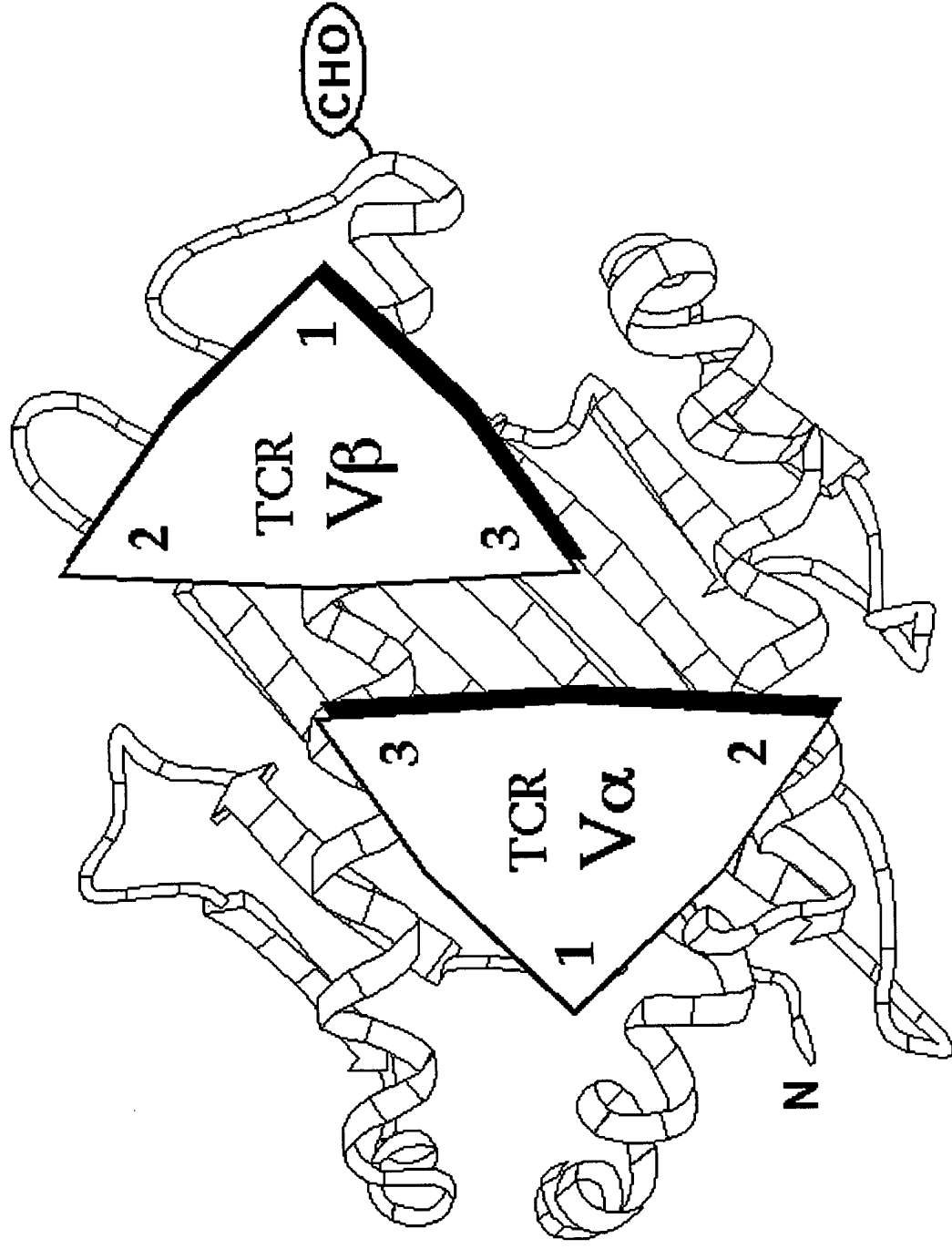


FIG. 5

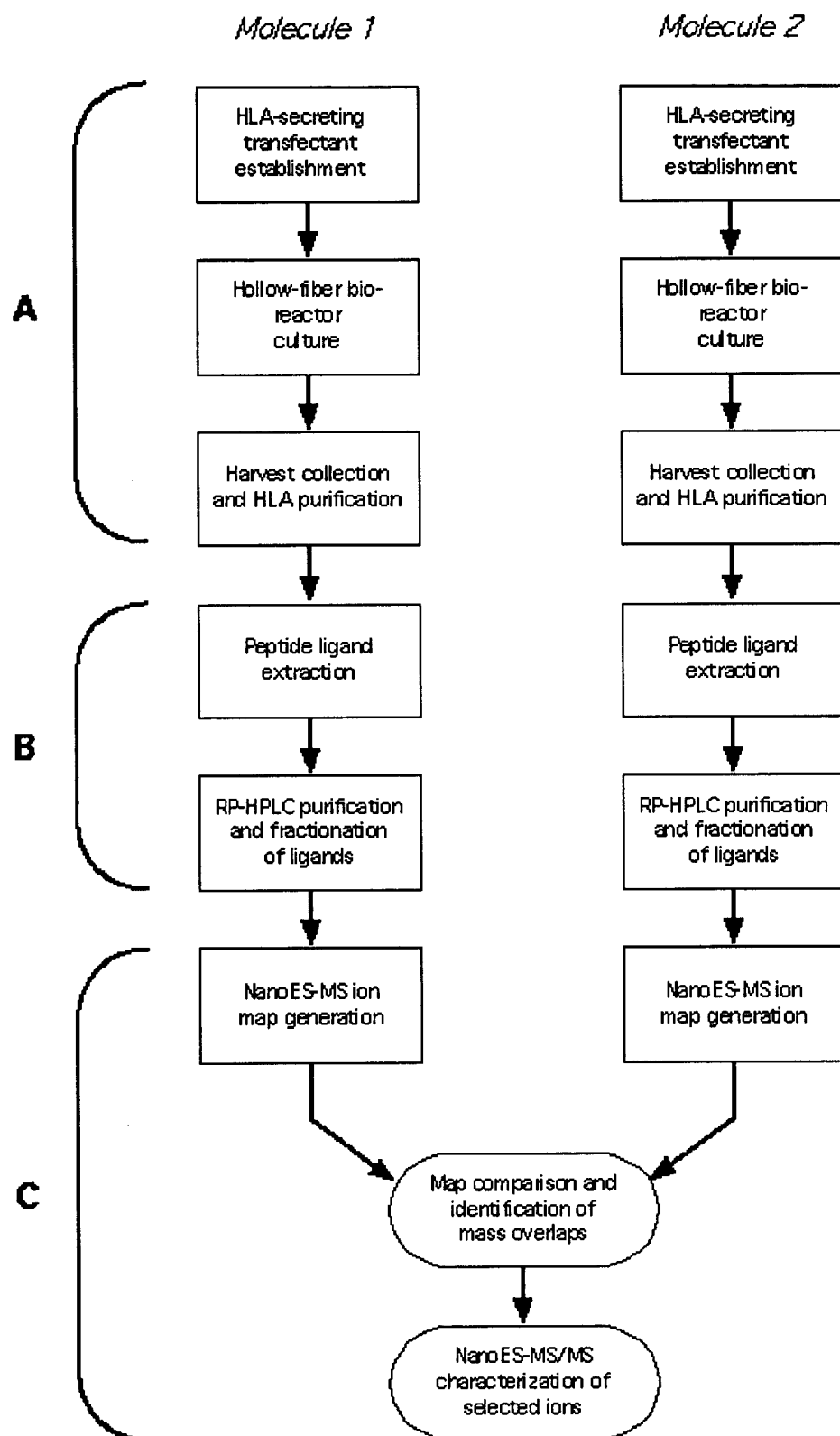


FIG. 6

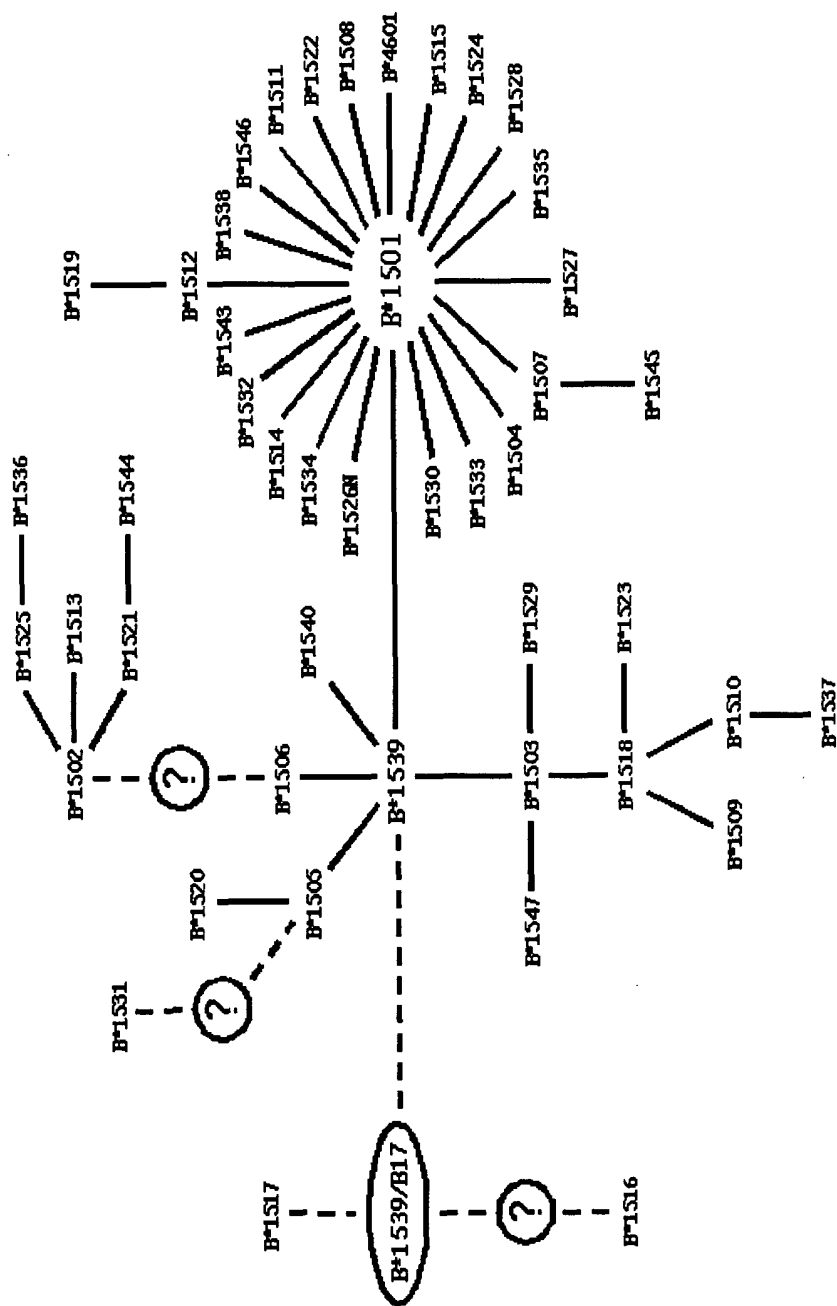


FIG. 7

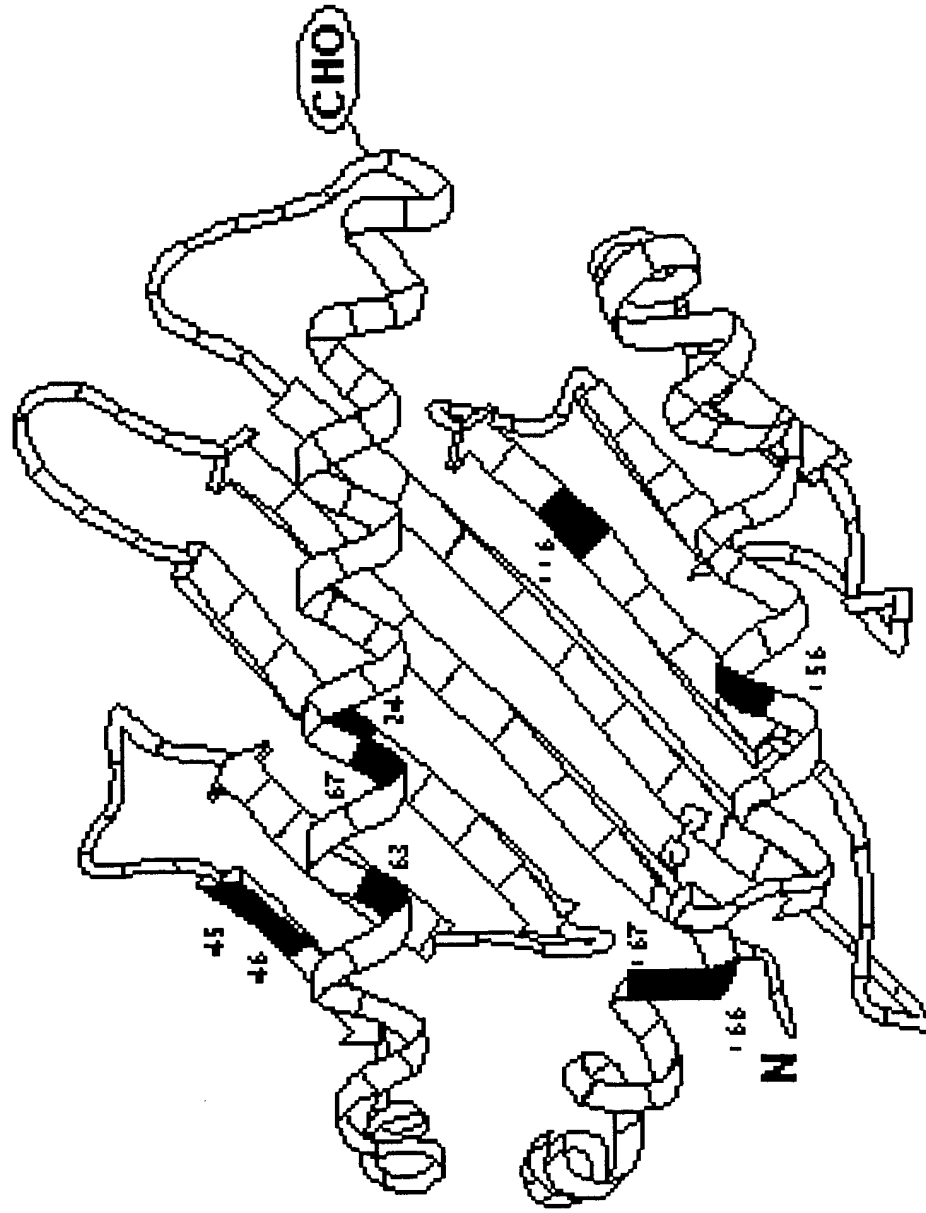


FIG. 8

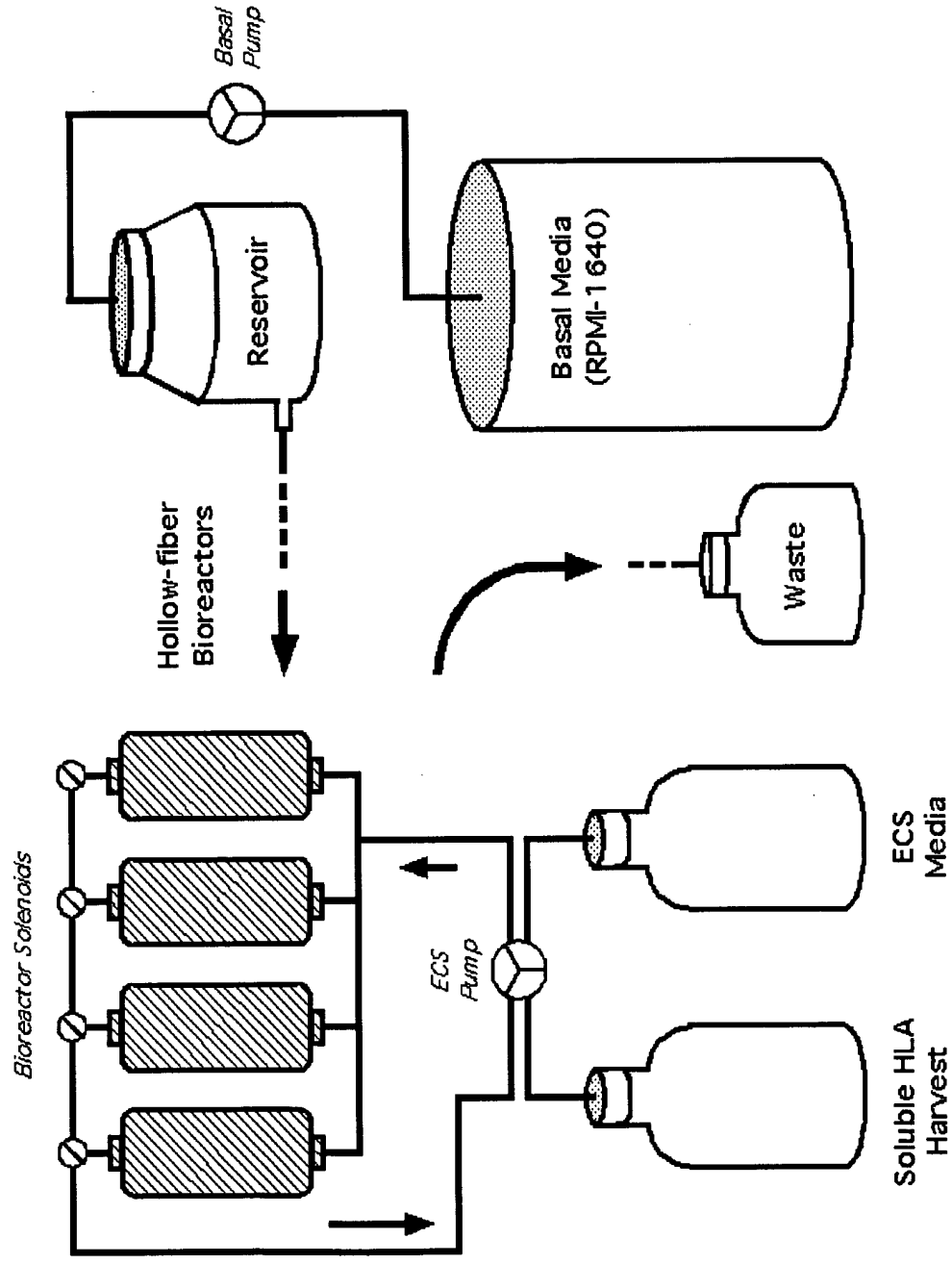
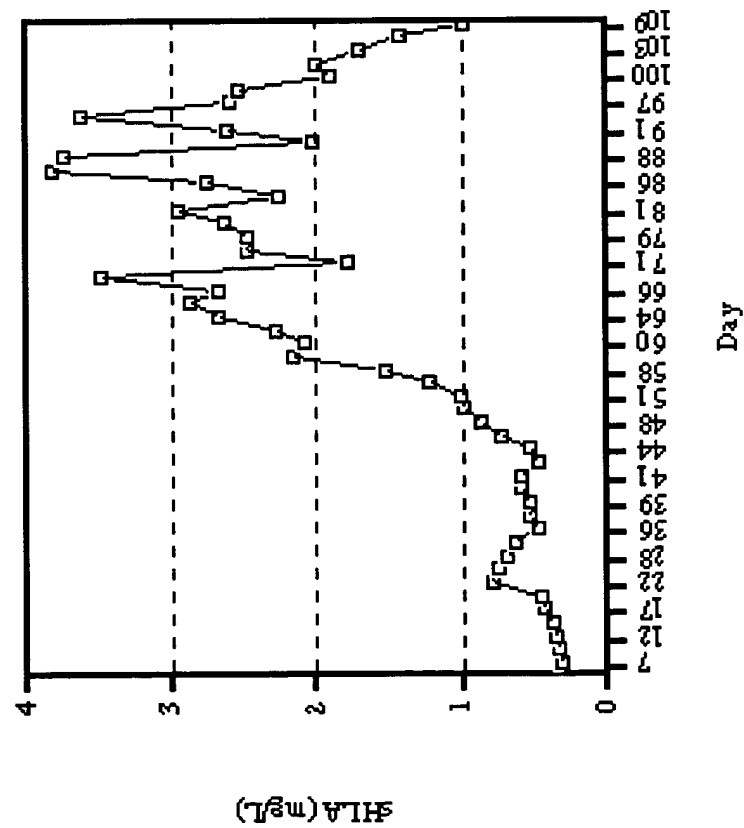


FIG. 9

B*1501T/PSR α -neo



B*1501T/pcDNA3

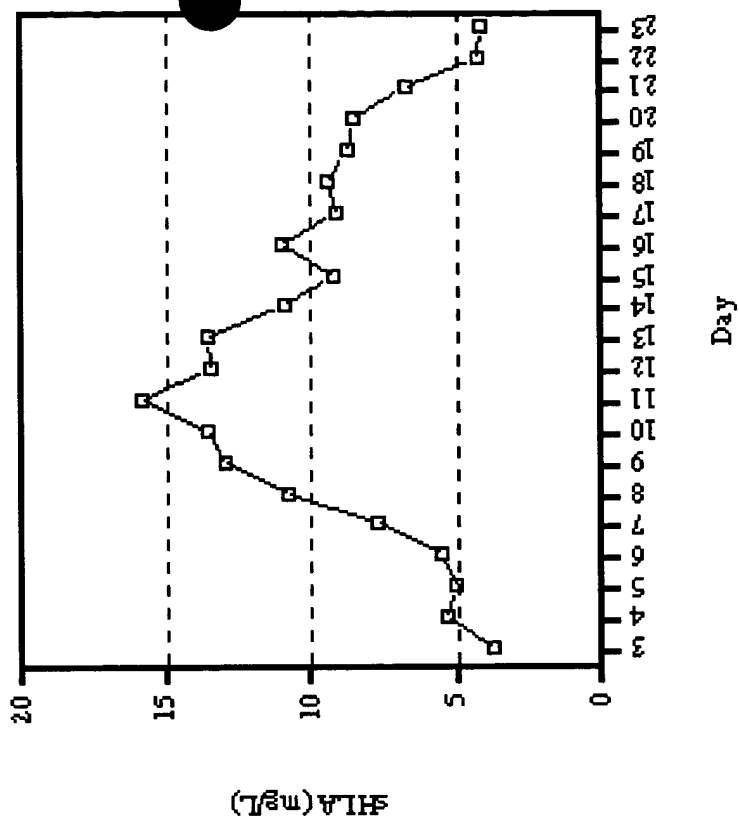


FIG. 10

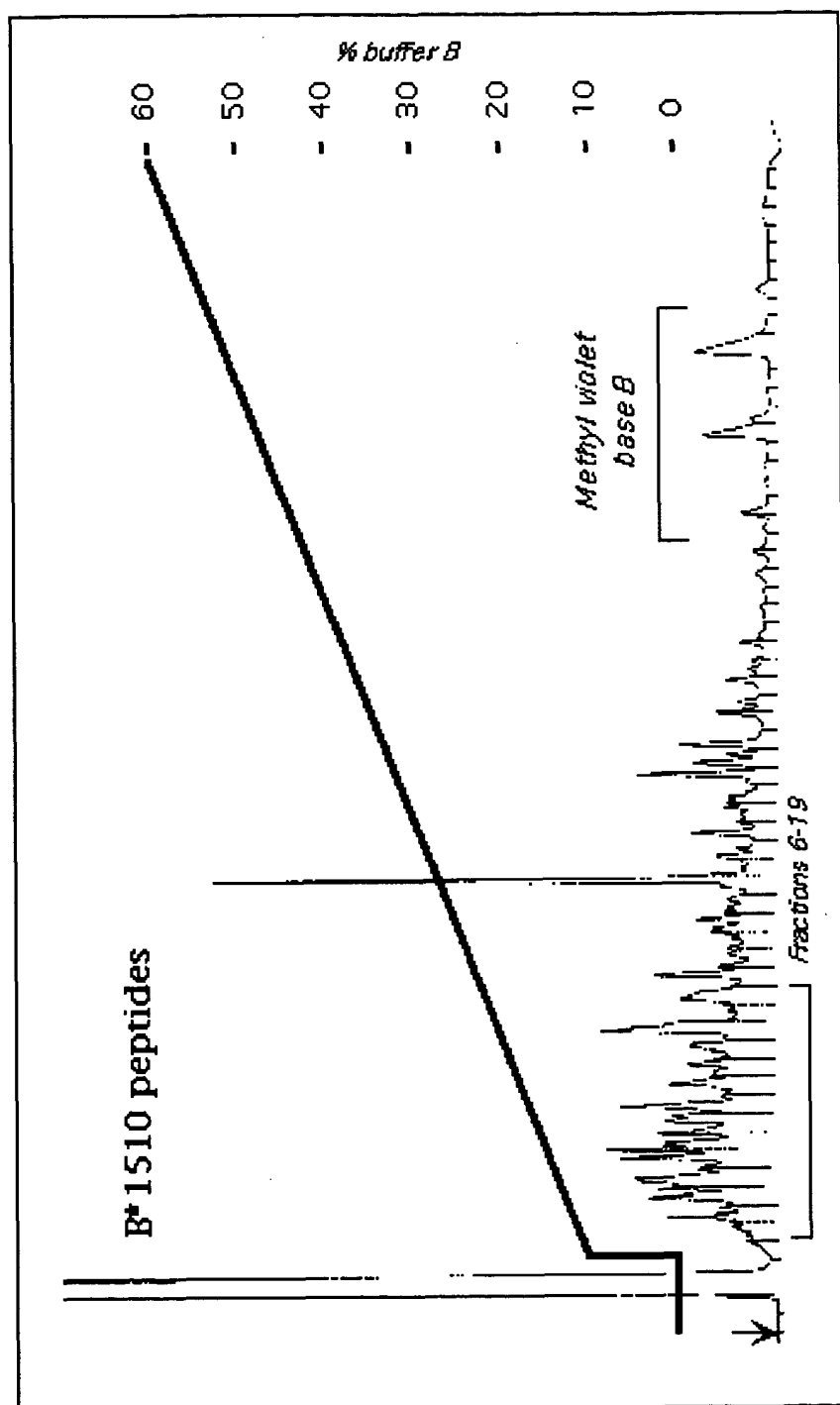
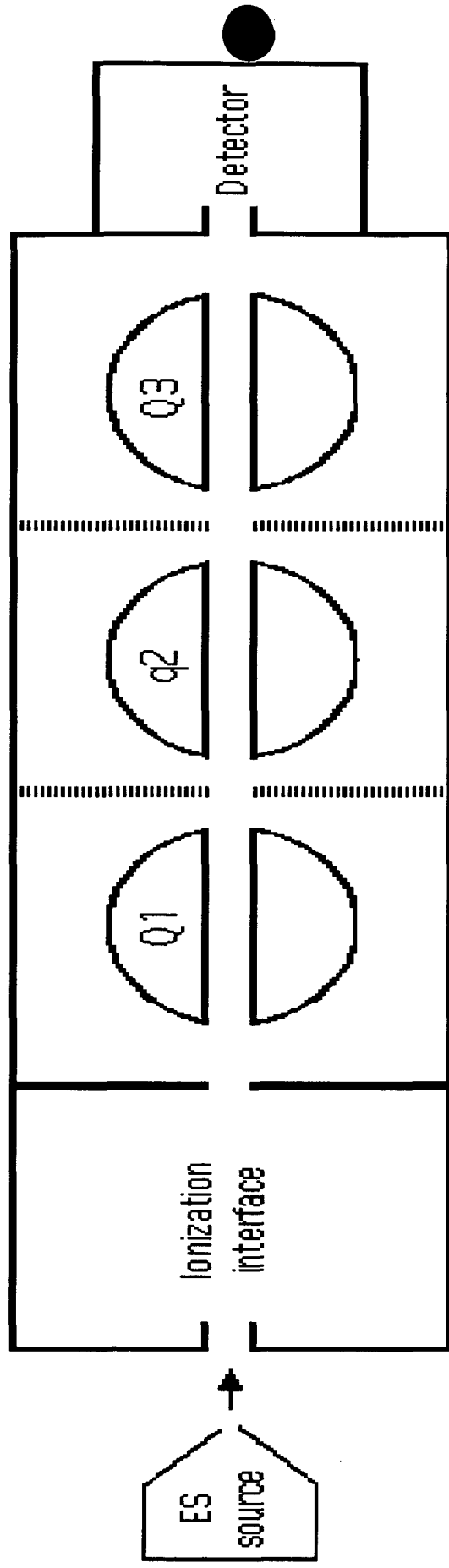


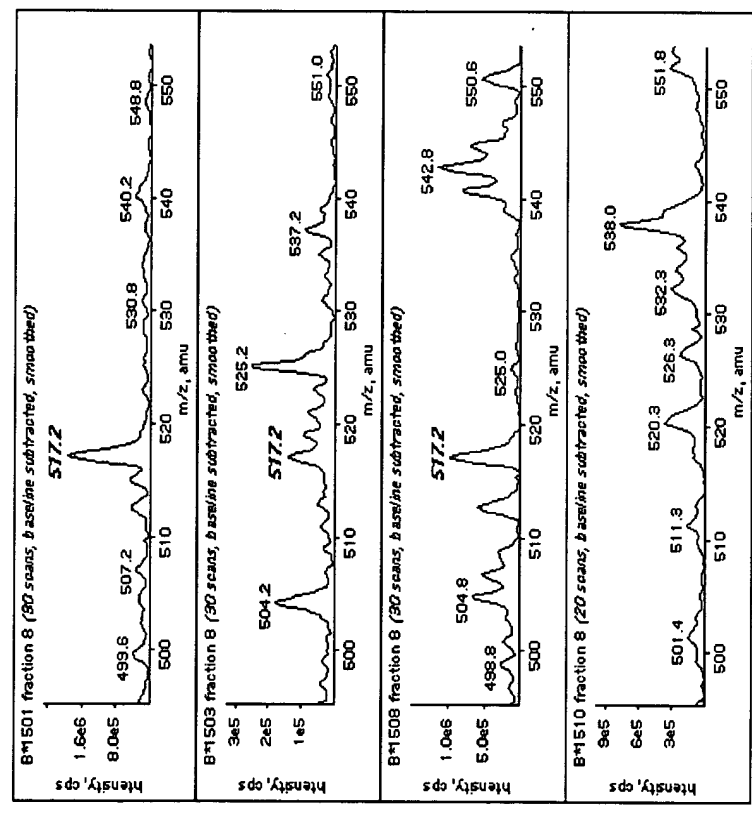
FIG. 11



Ion selection / transmission / collision

FIG. 12

A



C

y-ions: 9 8 7 6 5 4 3 2 1
1033 919 791 663 526 469 382 311 182
N Q Z H G S A E Y
b-ions: 1 2 3 4 5 6 7 8 9
116 243 371 508 565 652 723 862 1015

B

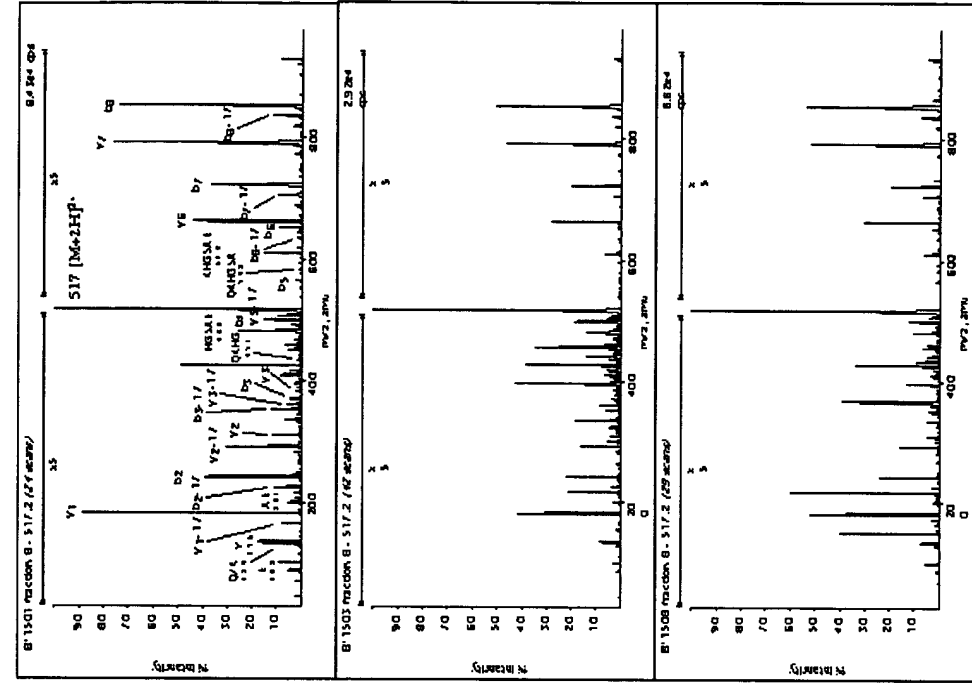
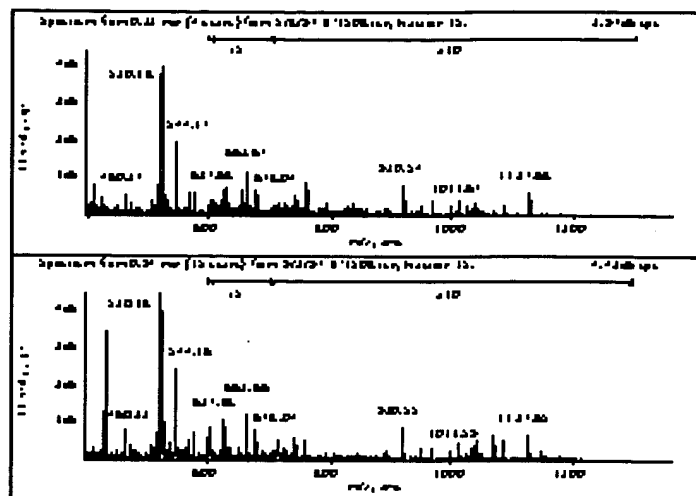
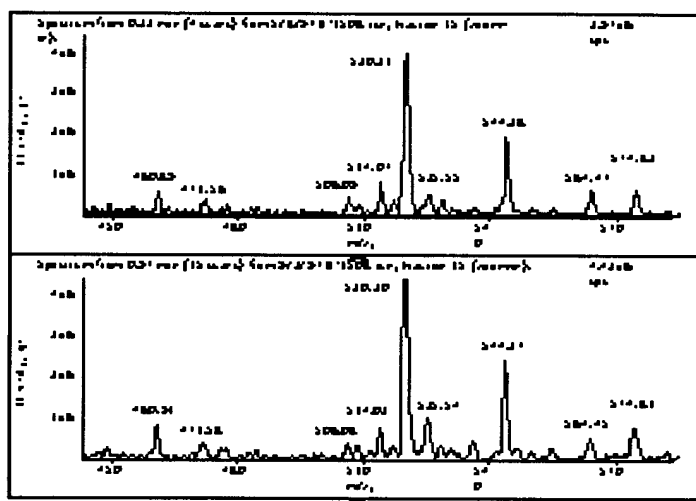


FIG. 13

A



B



C

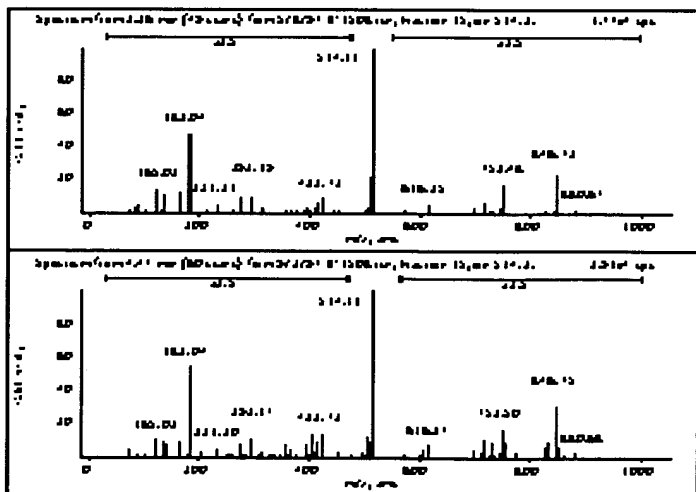


FIG. 14

A (W6/32-purified B*1501 complexes)

position:	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>dominant</i>	—	Q _(8.0)	K _(8.0)	—	—	—	—	—	Y _(4.0)	—	—	—	—	—
			F _(5.0)											
			R _(4.0)											
<i>strong</i>	—	M _(3.0)	Y _(3.0)	P _(2.5)	G _(2.0)	—	—	—	F _(3.0)	—	—	—	—	—
		L _(2.0)	P _(2.0)	D _(2.5)										
		V _(2.0)	N _(2.0)	G _(2.0)										
			H _(2.0)	E _(2.0)										

FIG. 15

B (BBM.1-purified B*1501 complexes)

position:	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>dominant</i>	—	Q _(7.5)	—	—	—	—	—	—	Y _(4.0)	—	—	—	—	—
<i>strong</i>	—	P _(3.5) L _(2.5) V _(2.0)	F _(2.5) K _(2.5) R _(2.0) P _(2.0) N _(2.0)	P _(3.2) D _(2.0) G _(2.0)	I _(2.0)	—	—	—	F _(3.0)	—	—	—	—	—

FIG. 15 CONT'D.

B*1508

B*1512

B*1503

B*1518

B* 1510

FIG. 16

10022066 121004

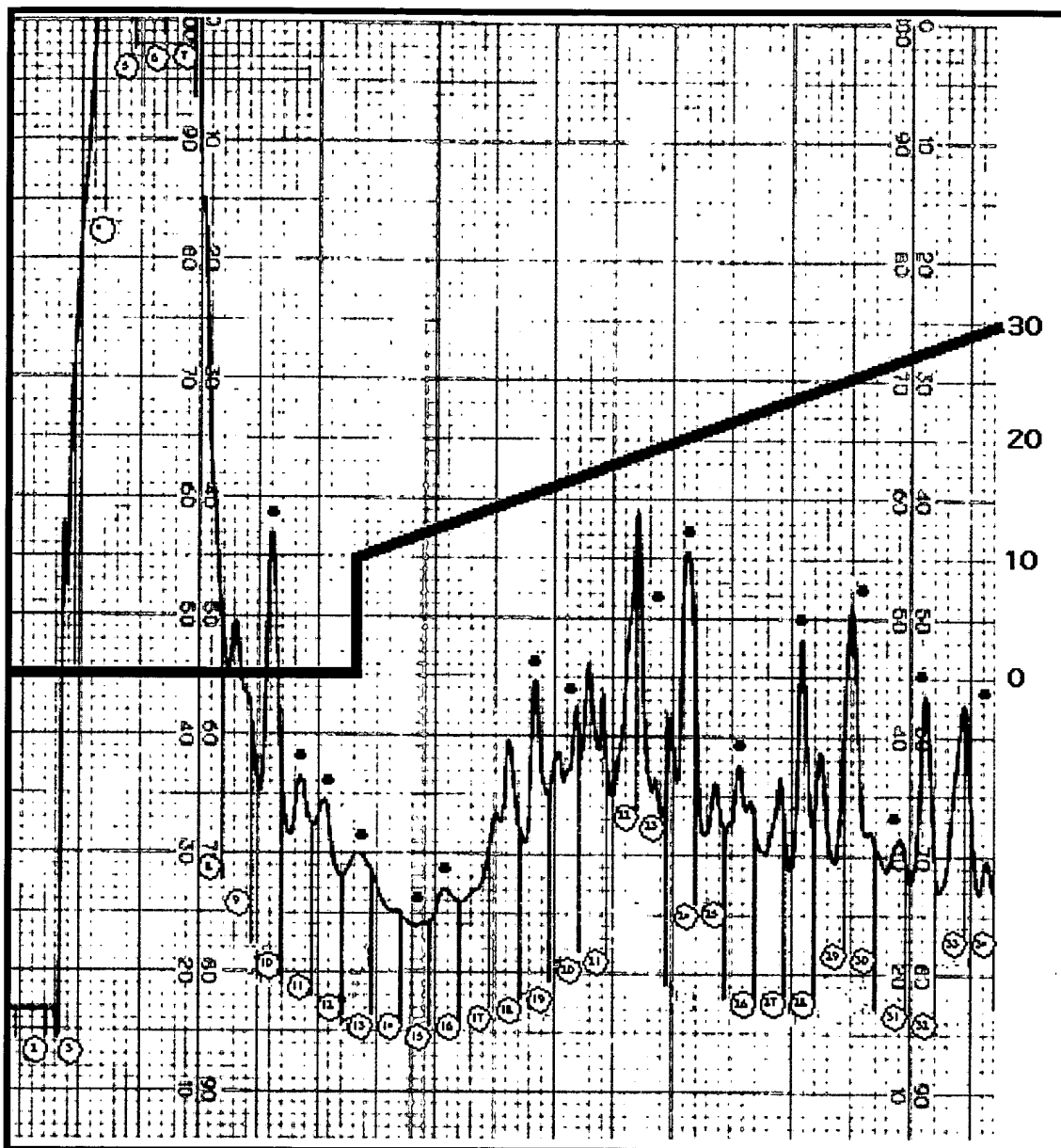


FIG. 17

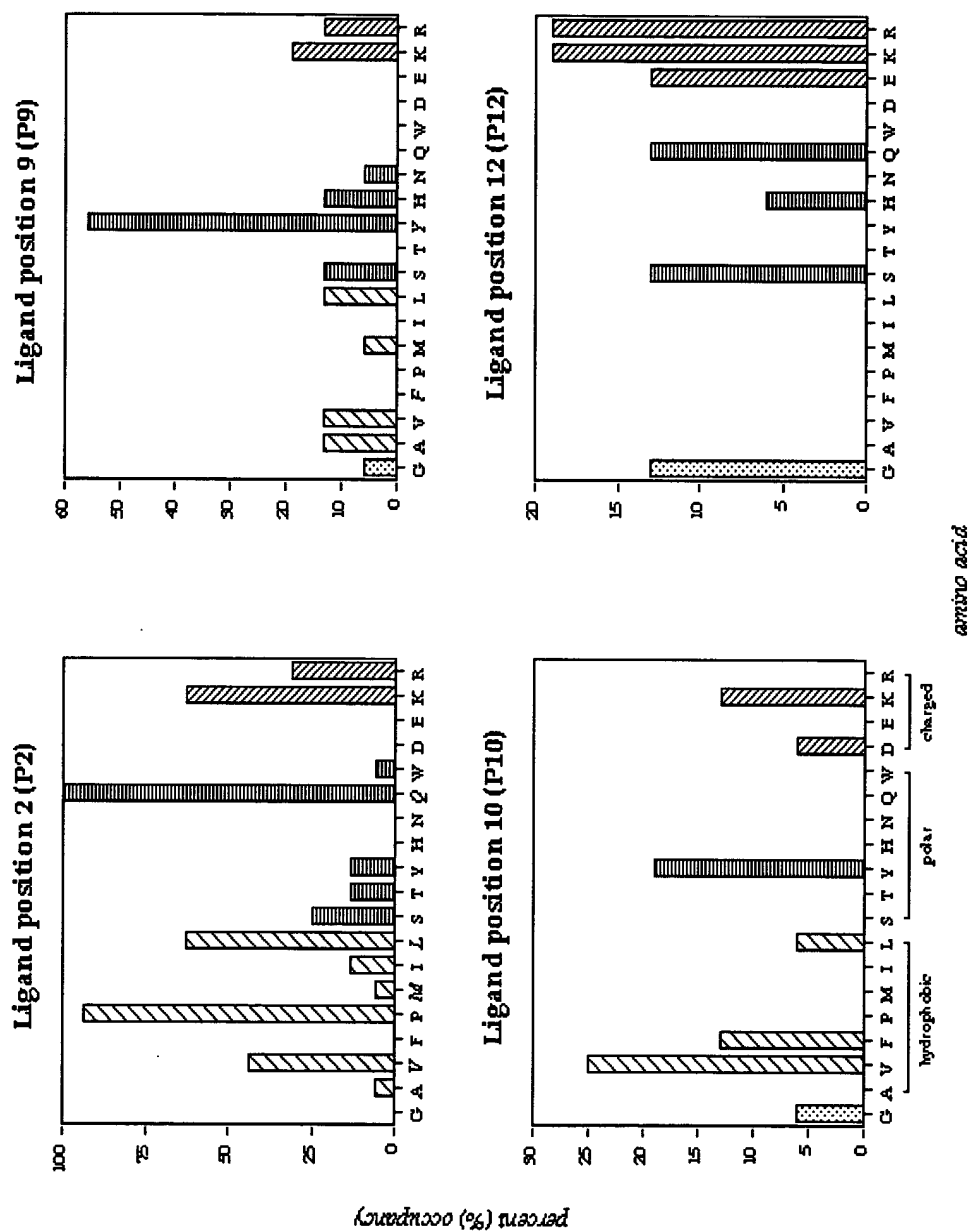


FIG. 18

Fraction 10

	2	3	4	5	6	7	8	9	10	11	12
<i>dominant</i>	P	-	-	-	-	-	-	-	-	-	-
	Q										
<i>strong</i>	W	K	G	-	-	-	-	-	-	-	-
<i>g</i>		R	F								
		H									
<i>weak</i>	S	E	D	S	H	V	I	Y	K	V	E
	I		N	W	S	T					
			M	P							
			I								

Fraction 15

	2	3	4	5	6	7	8	9	10	11	12
<i>dominant</i>	P	-	-	-	-	-	-	-	-	-	-
	Q										
<i>strong</i>	W	K	G	-	-	-	-	-	-	-	-
		R	F								
		H									
<i>weak</i>	S	E	D	S	H	V	I	Y	K	V	E
	I		N	W	S	T					
			M	P							
			I								

Fraction 28

position:	2	3	4	5	6	7	8	9	10	11	12
<i>dominant</i>	K	-	-	-	-	-	-	-	-	-	-
<i>strong</i>	Q	H	G	L	R	I	D	K	V	E	-
	V	N		S			N				
	P	R		H							
<i>weak</i>	-	P	E	P	V	P	Q	Y	-	F	S
		F		E	A	M	E	F		P	K
		K			F		A				
		D					H				
							W				

FIG. 19

[illegible]

Fraction 31										
position:	2	3	4	5	6	7	8	9	10	
<i>dominant</i>	-	K	-	W	-	-	-	-	-	
<i>strong</i>	S	H	N	R	S	F	-	G	F	
<i>g</i>	Q			M	Y	V				
	P									
<i>weak</i>	L	Y	A	-	L	-	Y	Y	-	
		L			K		S			
		V					K			

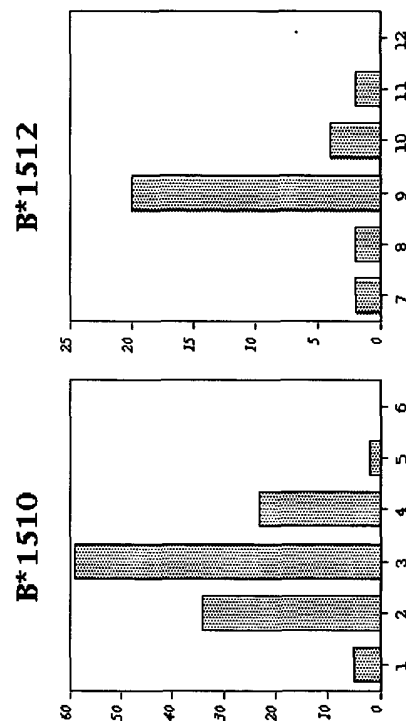
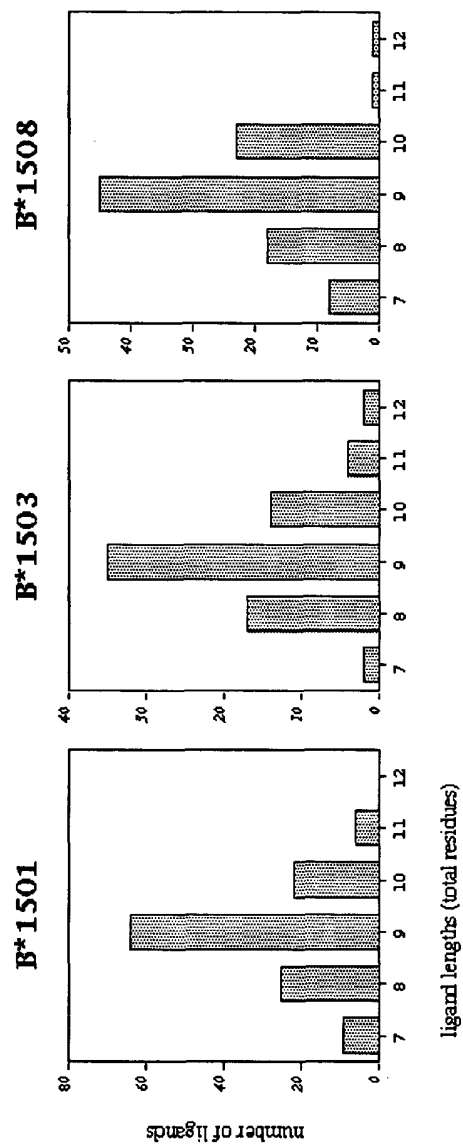


FIG. 20

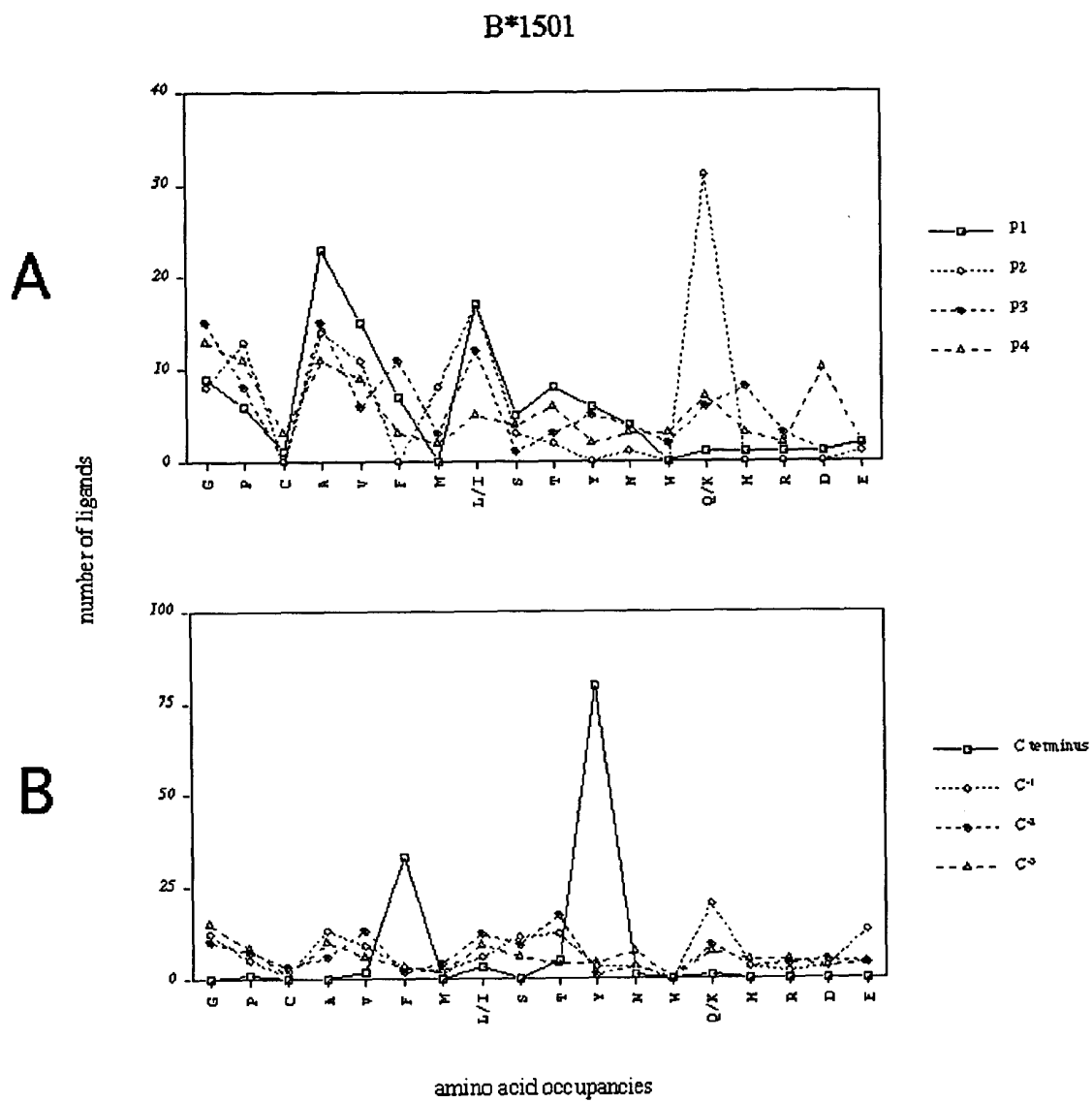
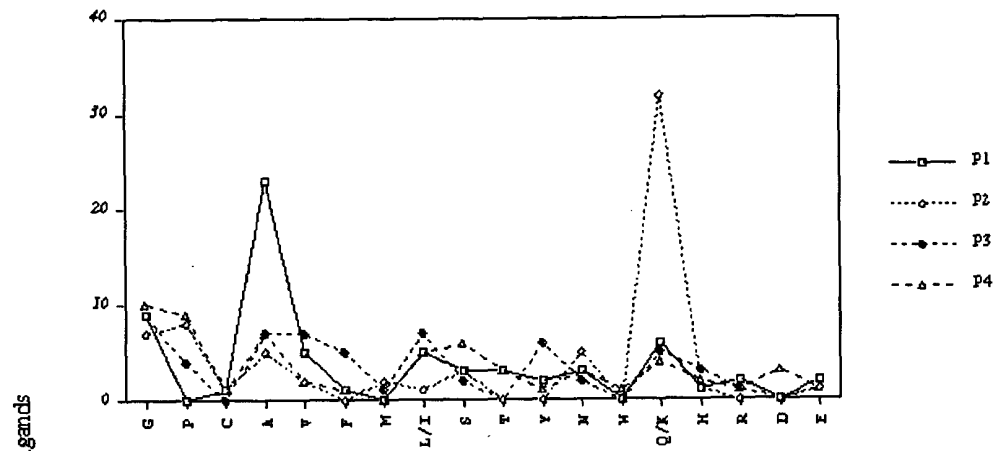


FIG. 21

B*1503

A



B

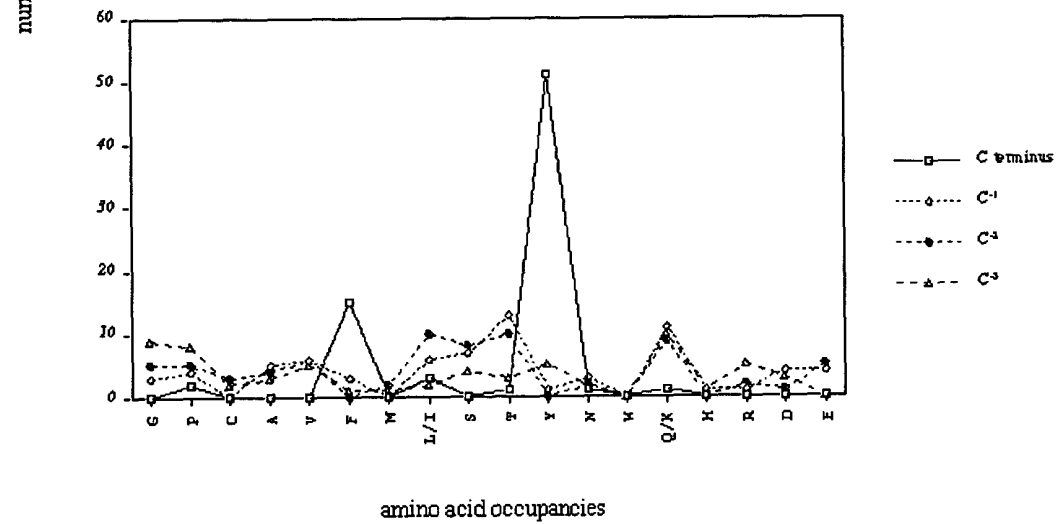
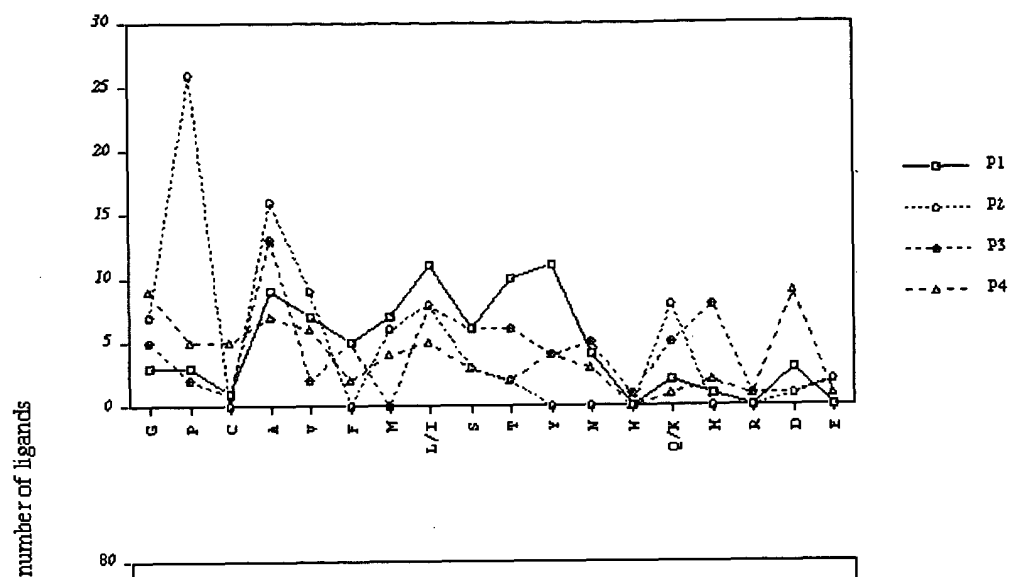


FIG. 22

B*1508

A



B

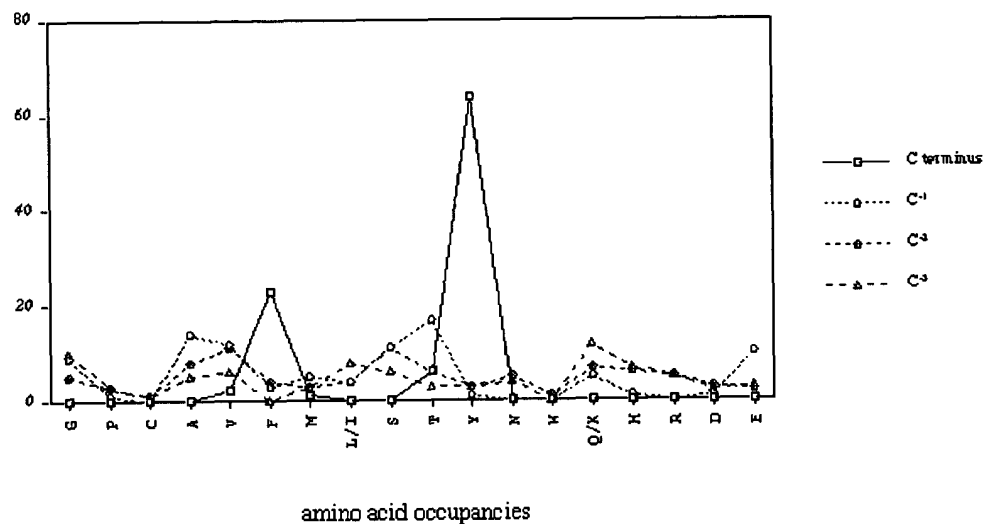
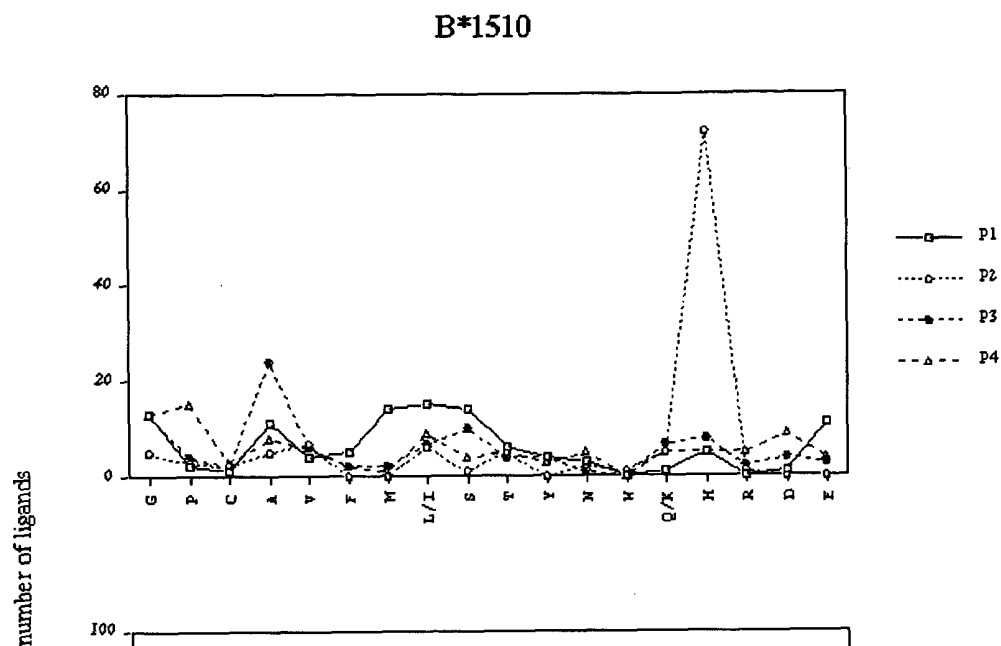


FIG. 23

A



B

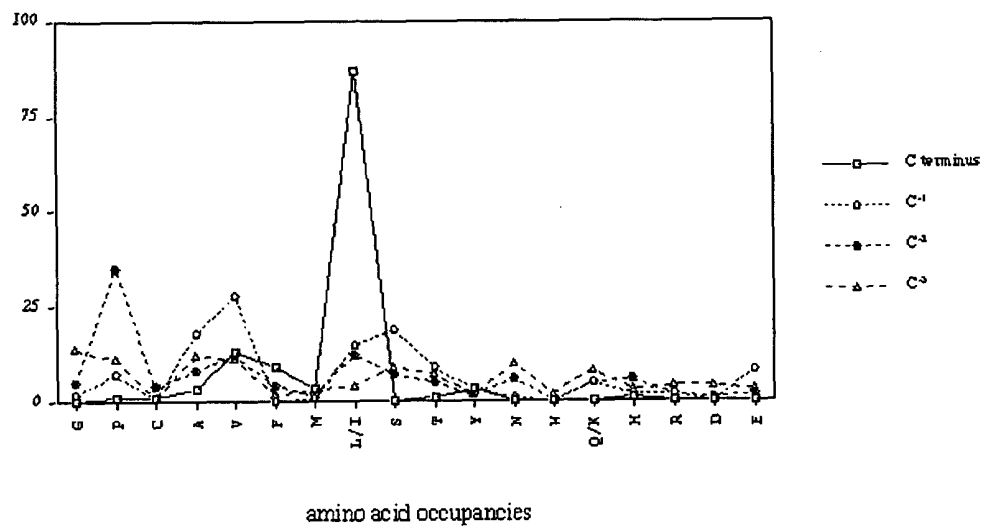
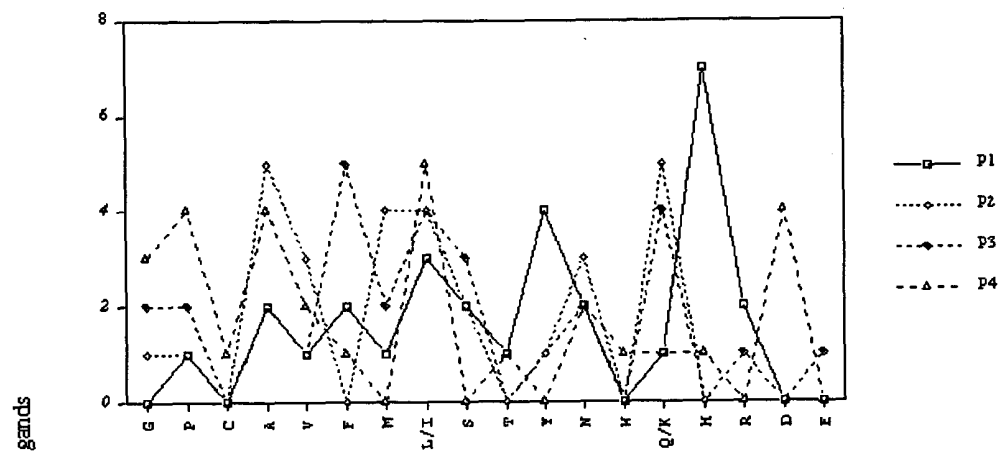


FIG. 24

B*1512

A



B

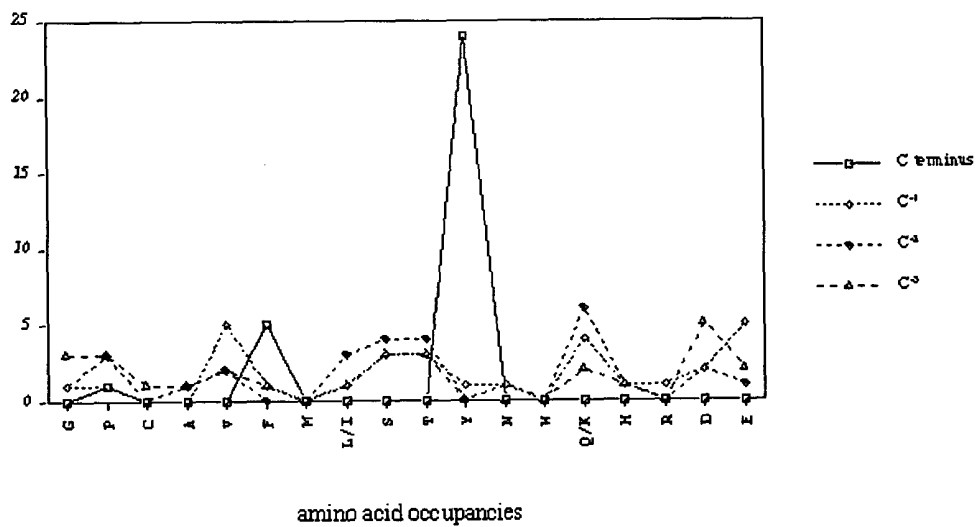
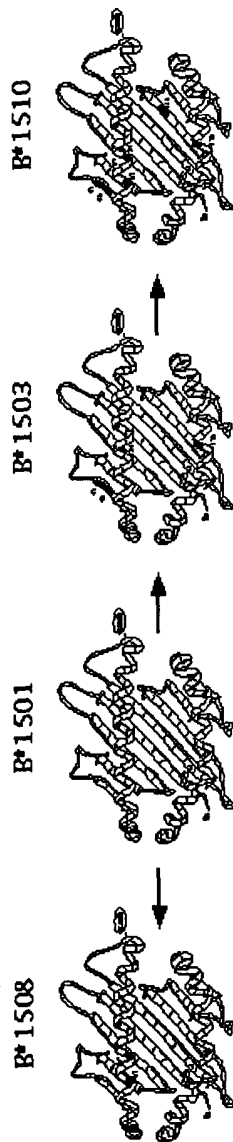


FIG. 25



```

--MGRMTXF
--Y
GSHGVAY
TG----AY
FVSNHAY
SQFDNVTY
XAN--YT
FLAMZSTY
WVXDSZTY
VWACV---Y
PLA-N-KTY
VVARPTVGY
FOARXTEY
VGVVDOTOF
--XVEF
TRVXSVEY
ARFCG---XV
YLM--ET
ILGPPGGSY
XLGDMWNY
YMDIPSGVSY

```

```

MQZHGSAEY
TPXGEFYZSY
SQFGGGSQY
CPLSCFT

```

```

AQFASGAGZ
--G--CDY
APWARGZY
GQZAVIF
NPPAZIPN
--Q--DPPDMTY
GQKAGASVF
AEFMACTY

```

FIG. 26

B*1508



1 2 3 4 5 6 7 8 9

B*1501

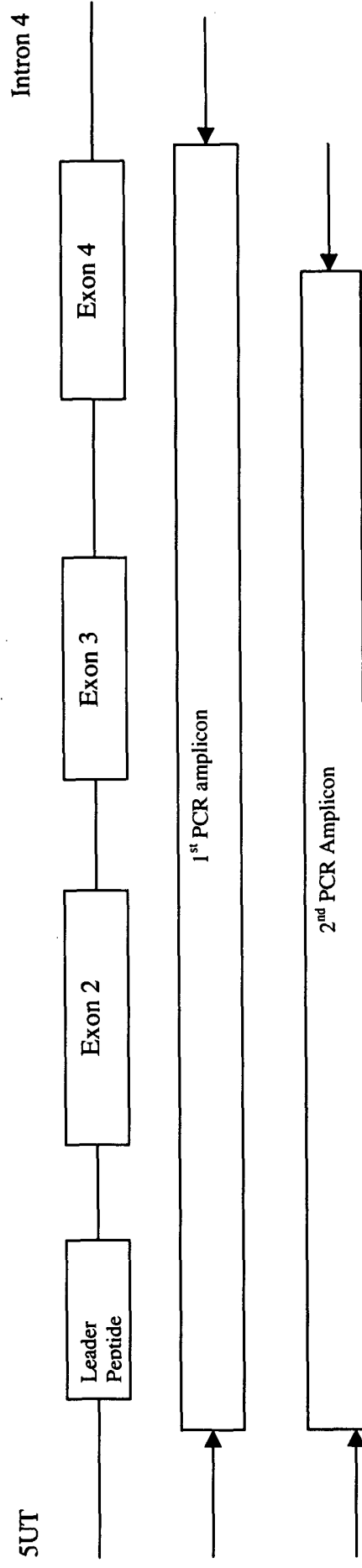


B*1503



FIG. 27

FIG. 29 PCR Strategy



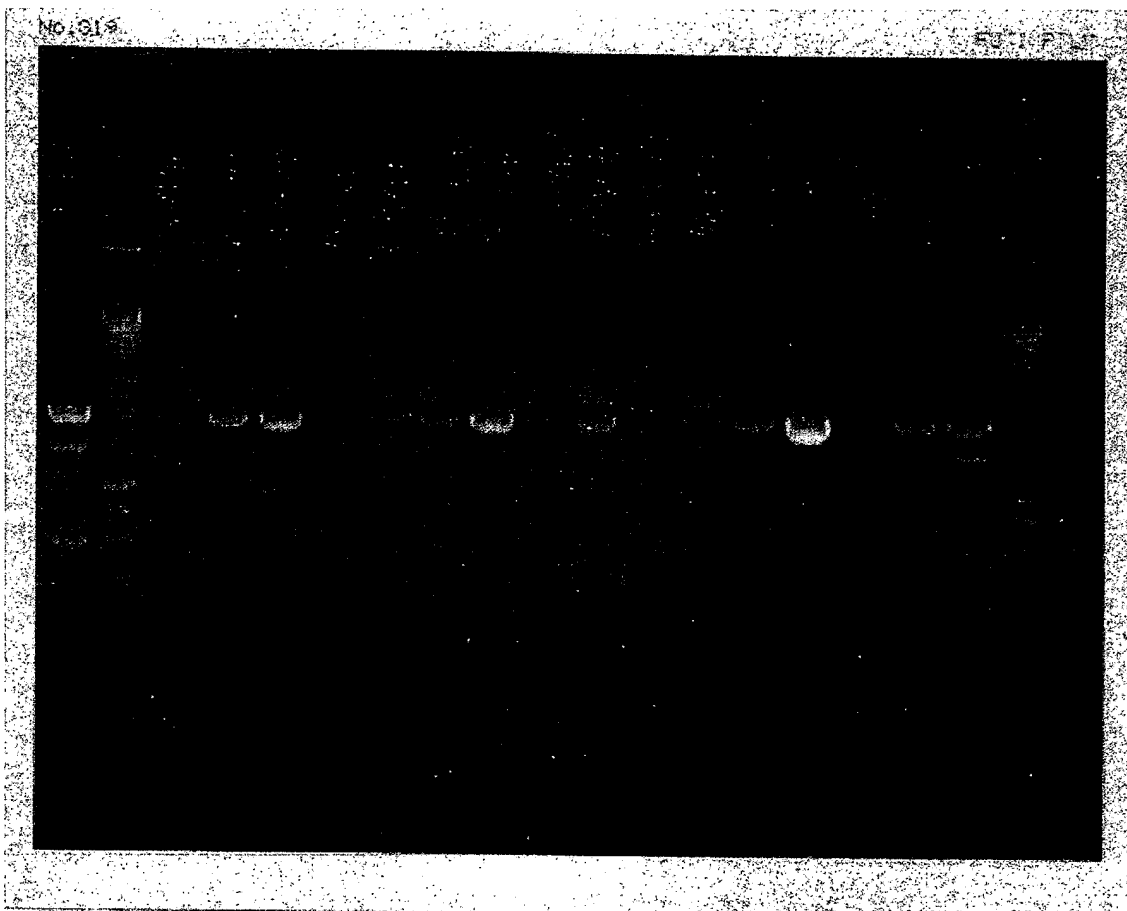


FIG. 30

BEST AVAILABLE COPY

No. 339

FUJI FILM

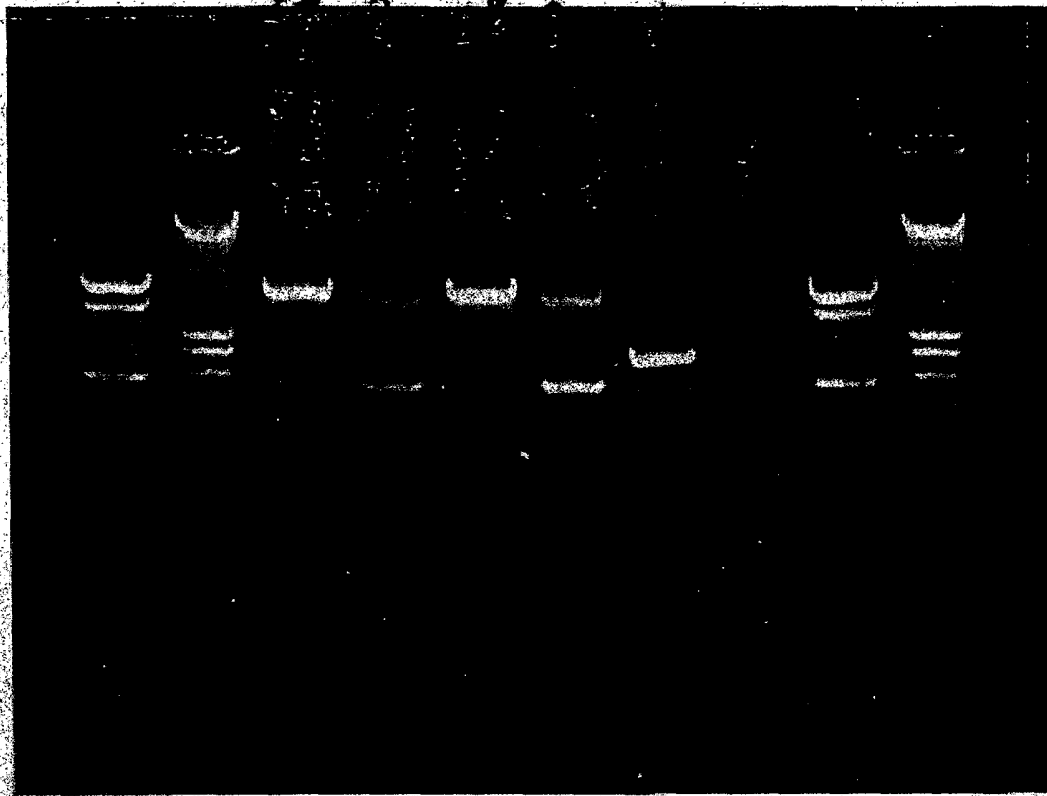


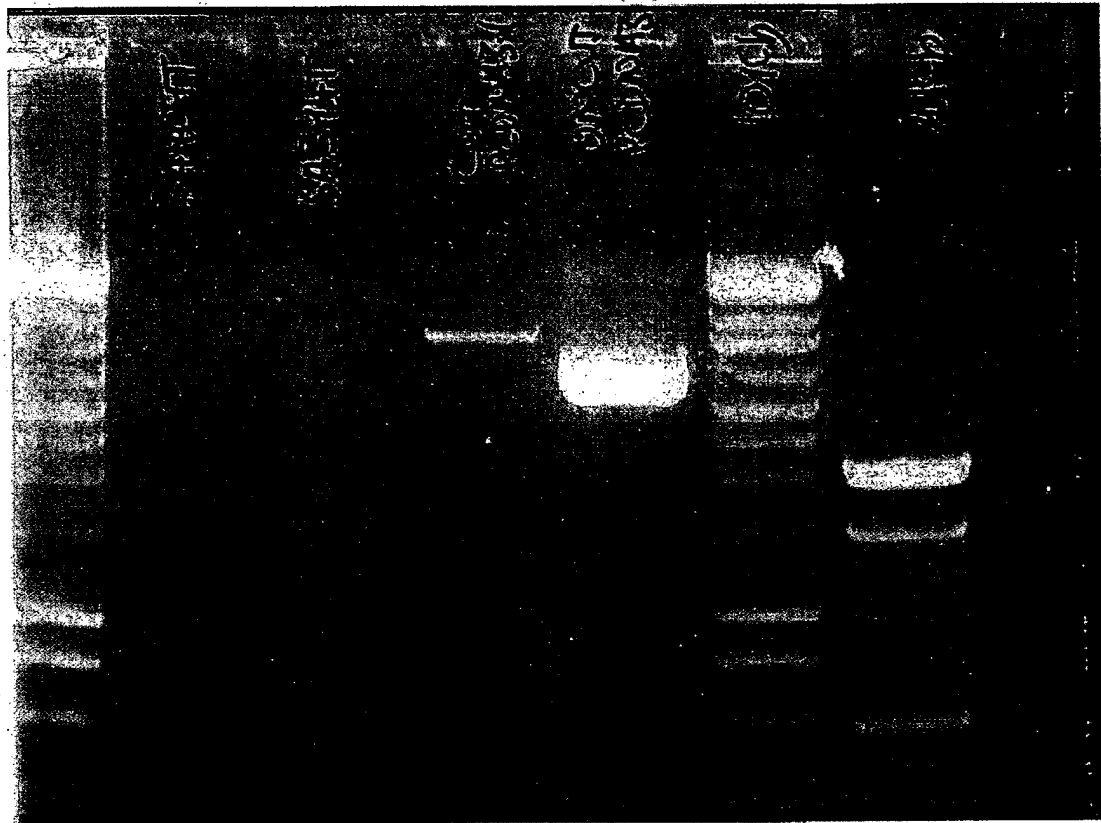
FIG. 31

BEST AVAILABLE COPY

FOOTNOTES: 99000000

No. 352

FUJI FILM



1 hour 0.8% Gel

FIG. 32

GDNA FIG. 5

BEST AVAILABLE COPY

No. 368

3A394T PC 1-12

FUJI FILM

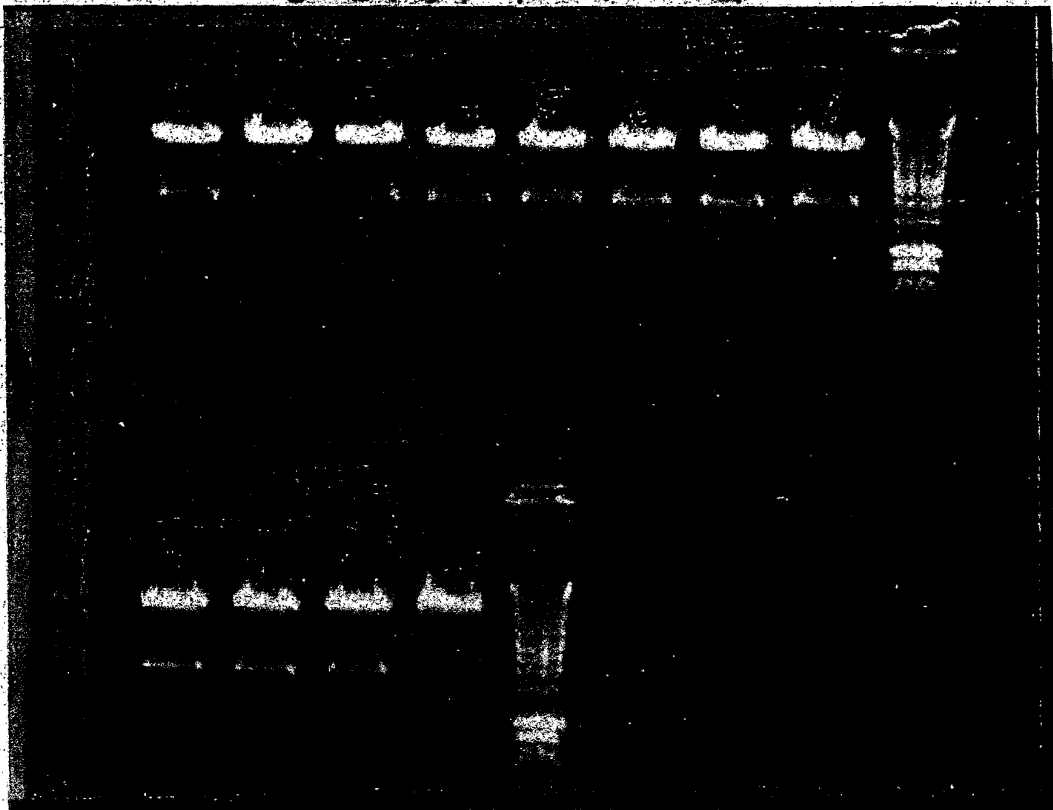


FIG. 33

BEST AVAILABLE COPY

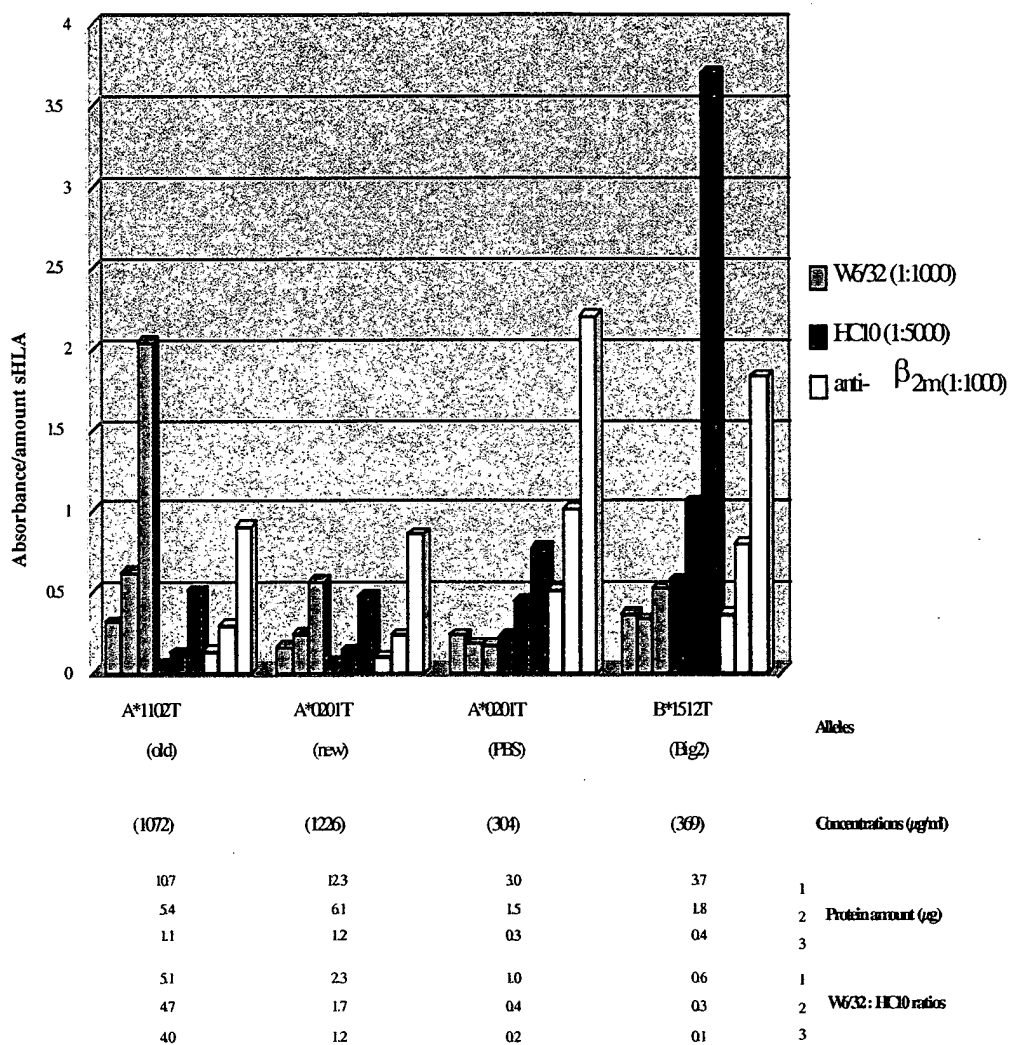


FIG. 34

BEST AVAILABLE COPY

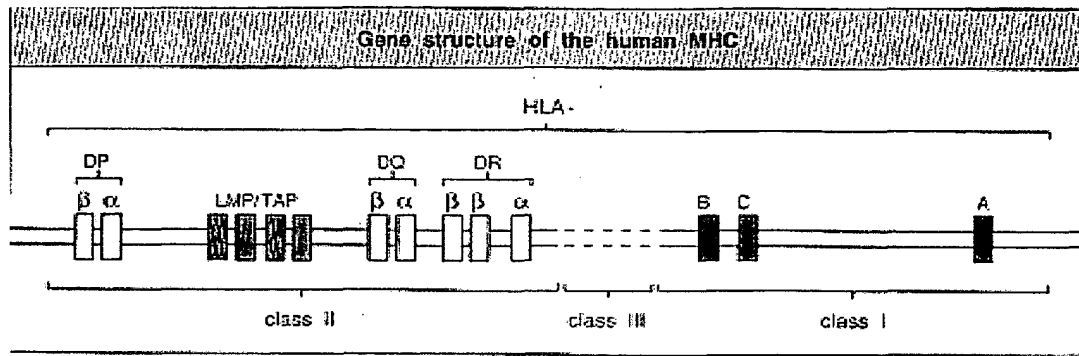


FIG. 35

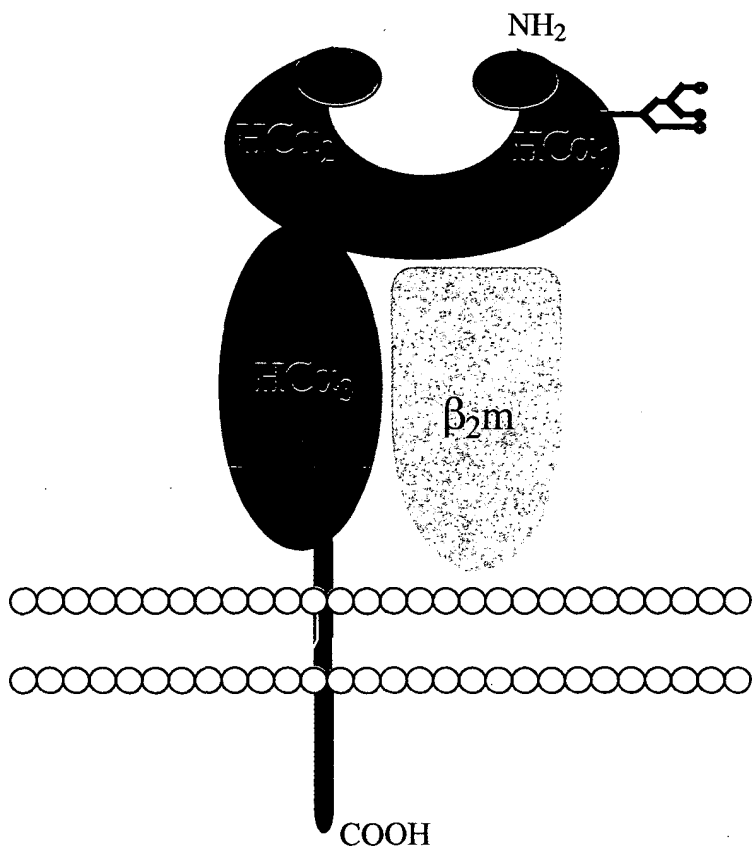


FIG. 36

BEST AVAILABLE COPY

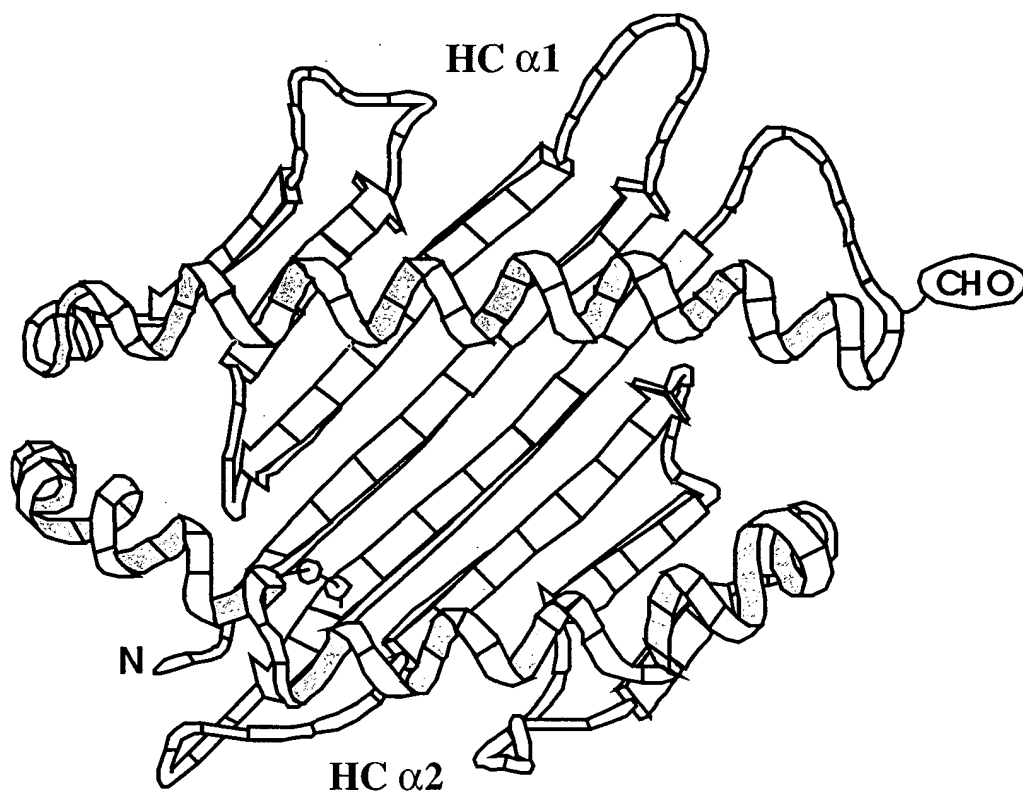


FIG. 37

BEST AVAILABLE COPY

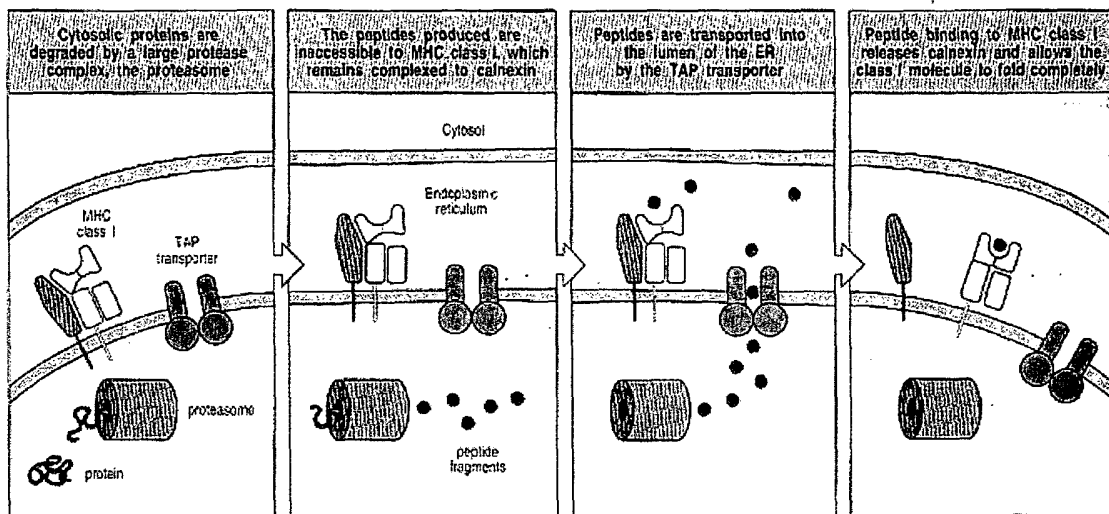


FIG. 38

BEST AVAILABLE COPY

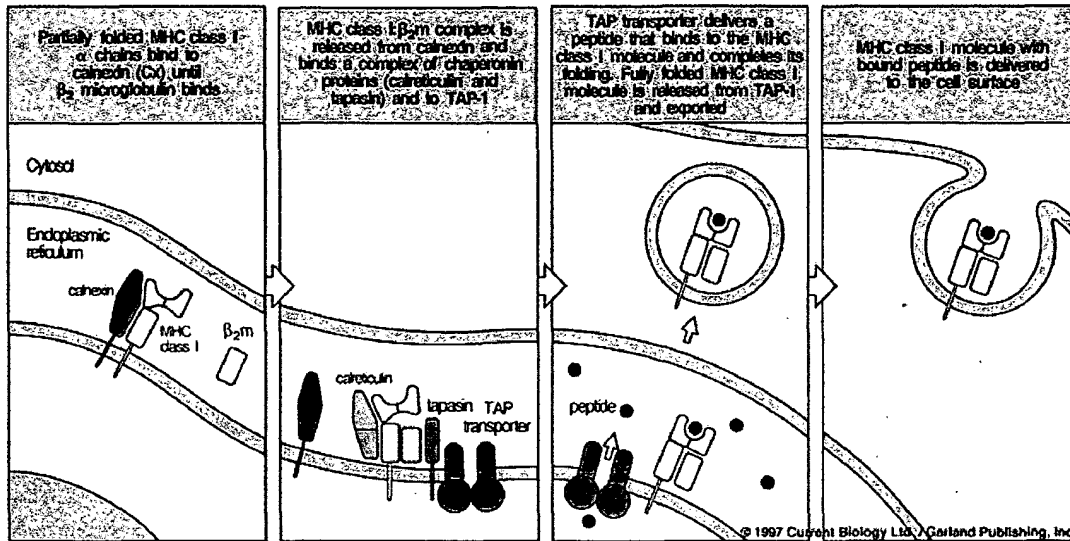


FIG. 39

BEST AVAILABLE COPY

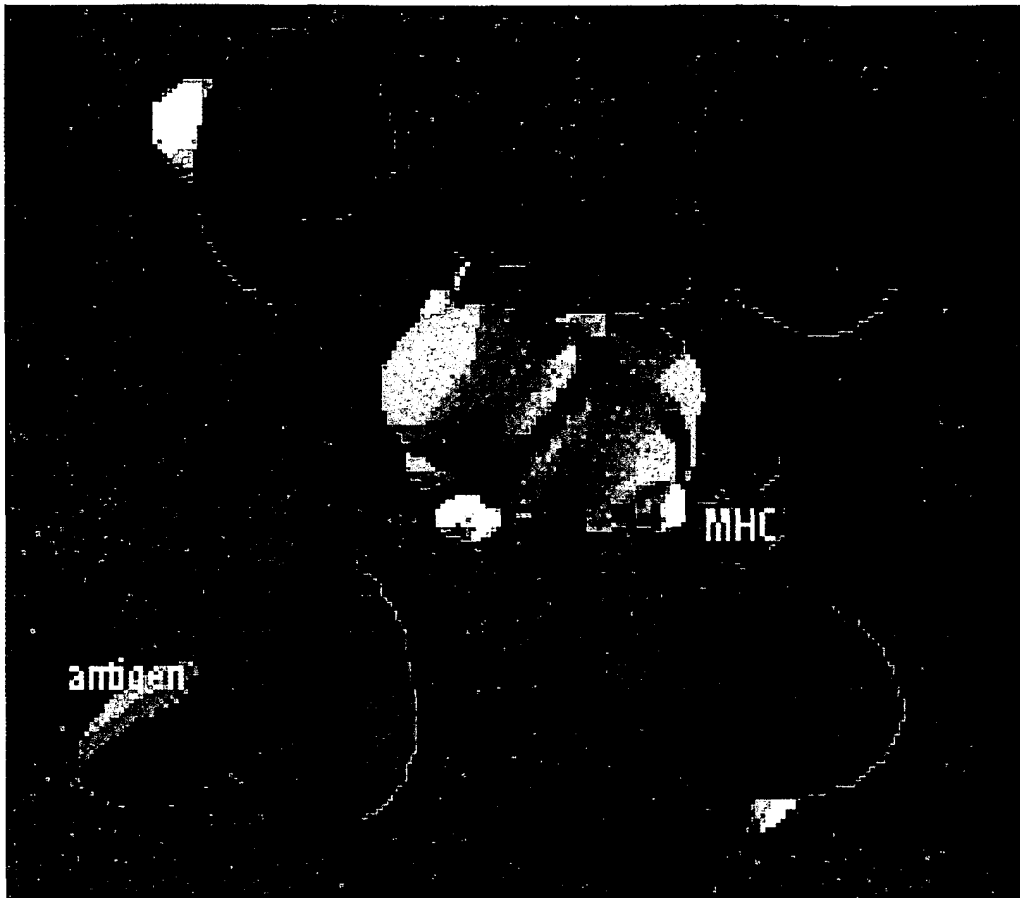
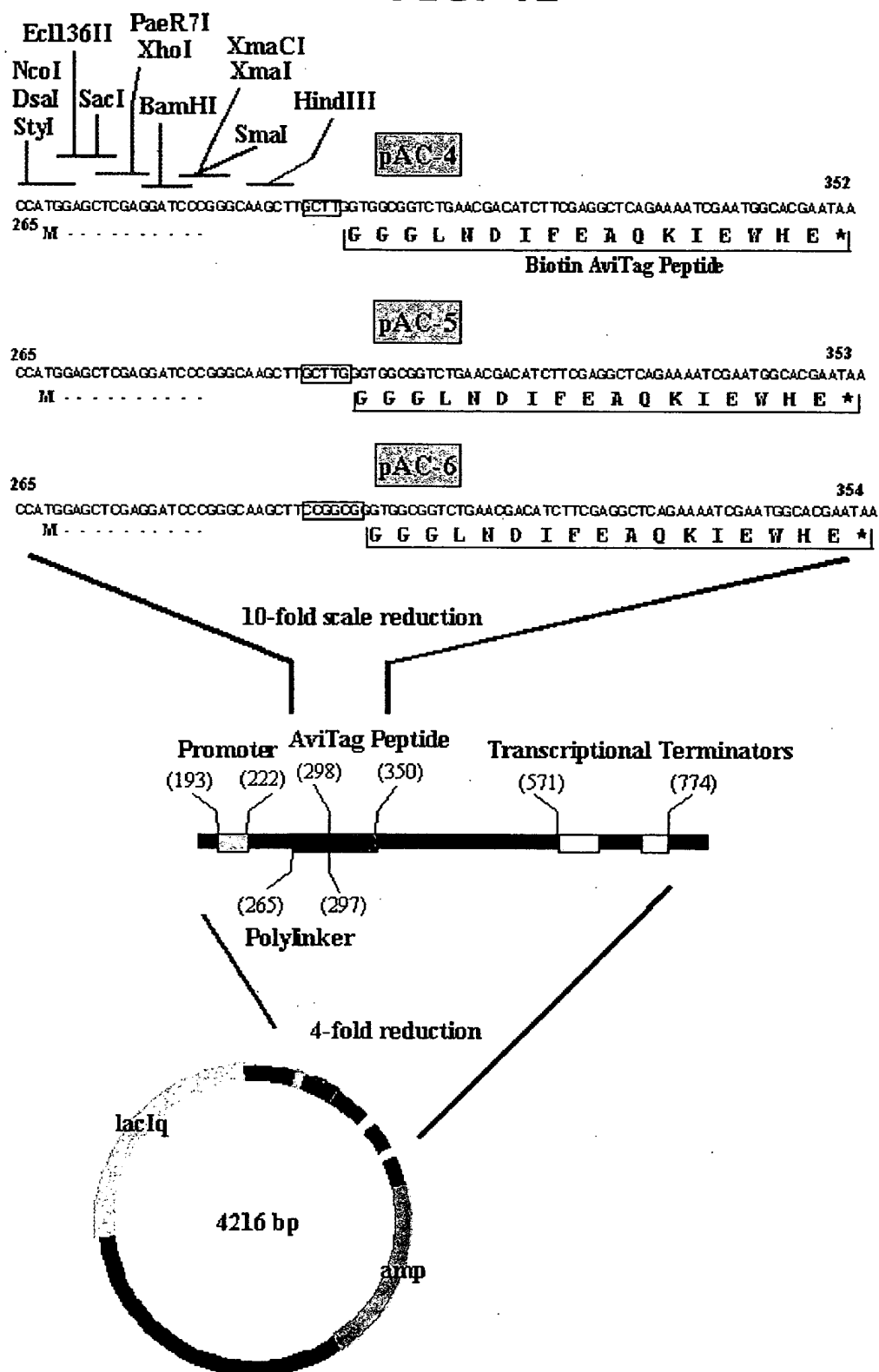


FIG. 40

BEST AVAILABLE COPY

FIG. 41



BEST AVAILABLE COPY

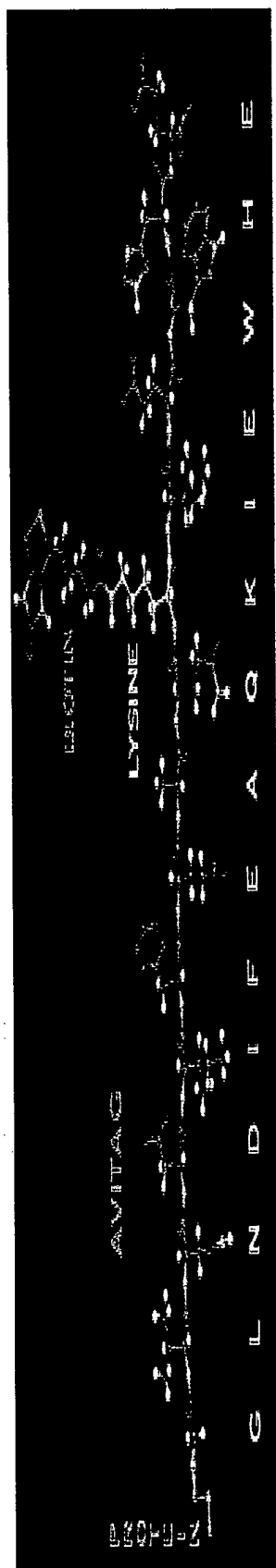
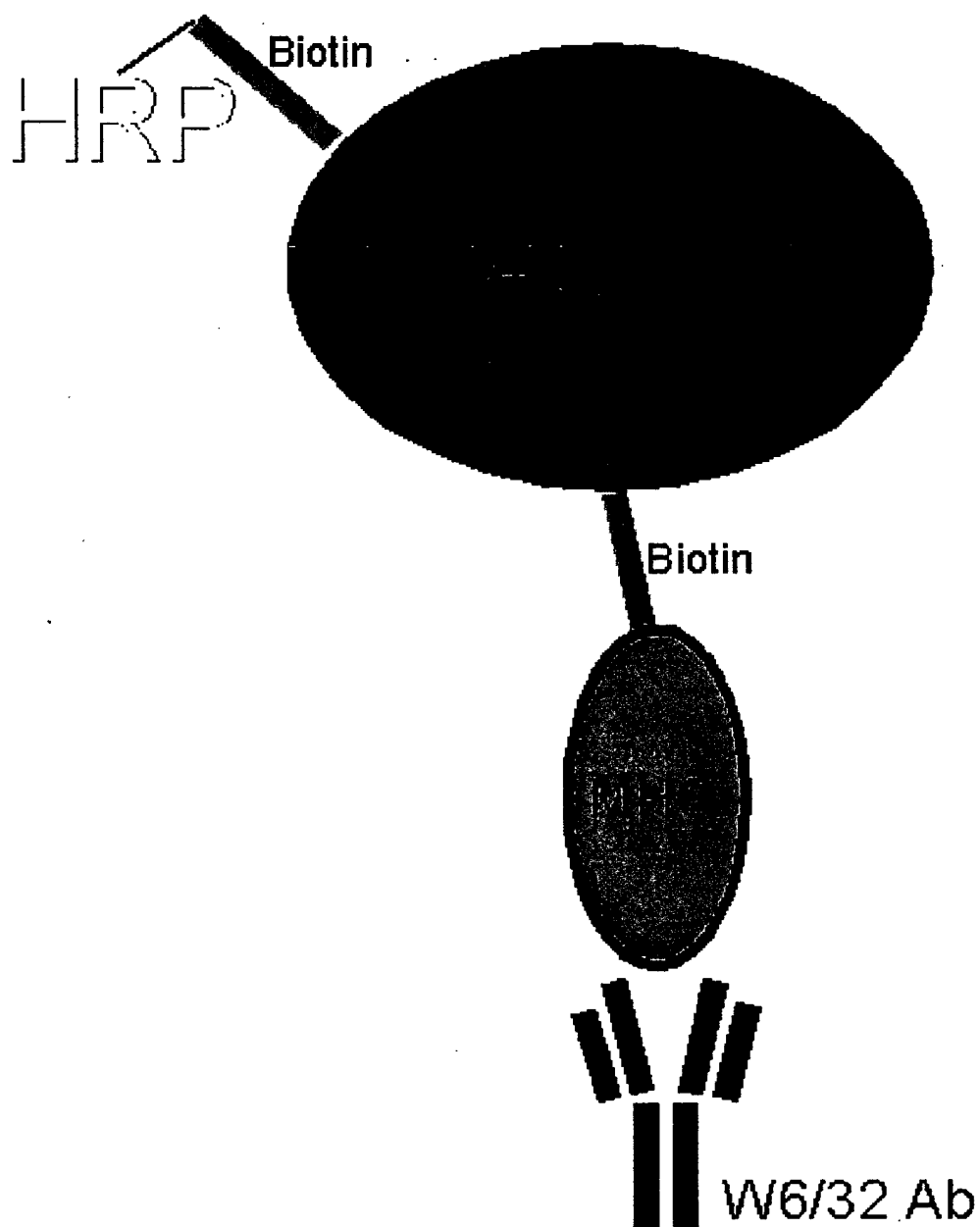


FIG. 42

FIG. 43



BEST AVAILABLE COPY

sHLA-B*0702 PRODUCTION BY T2 TRANSFECTANTS AFTER PEPTIDE PULSING

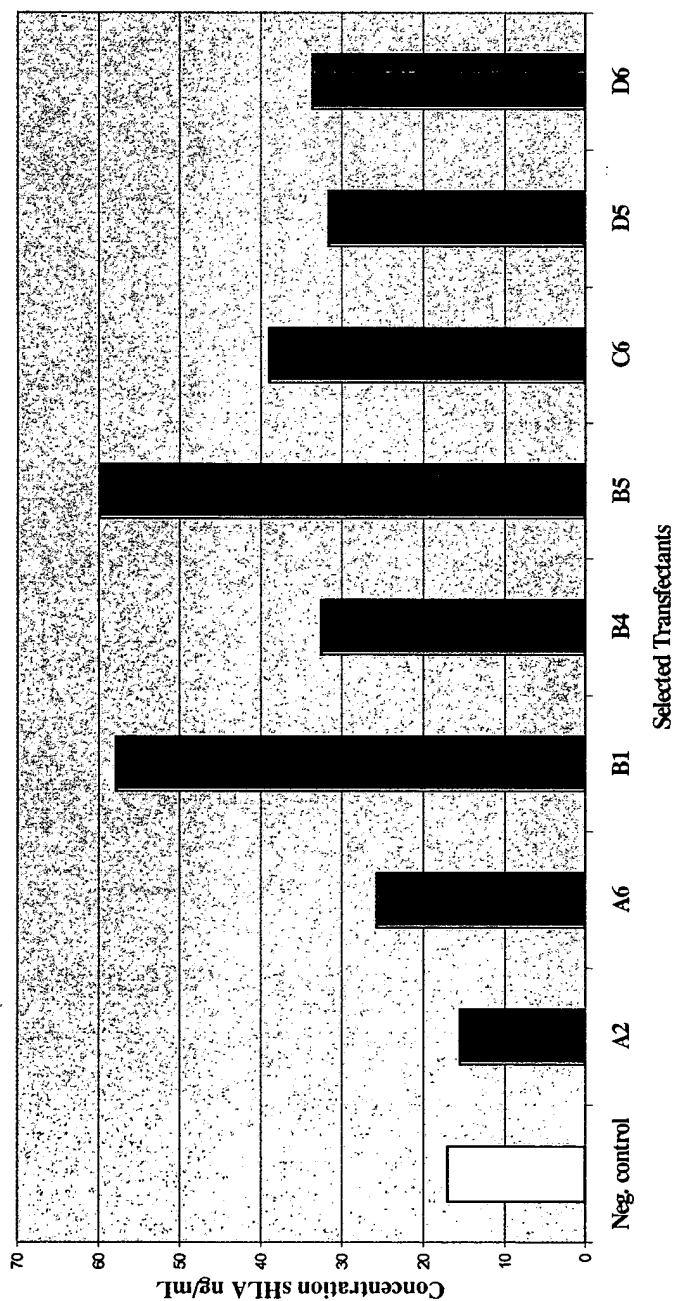


FIG. 44

sHLA Purification Elution Curve

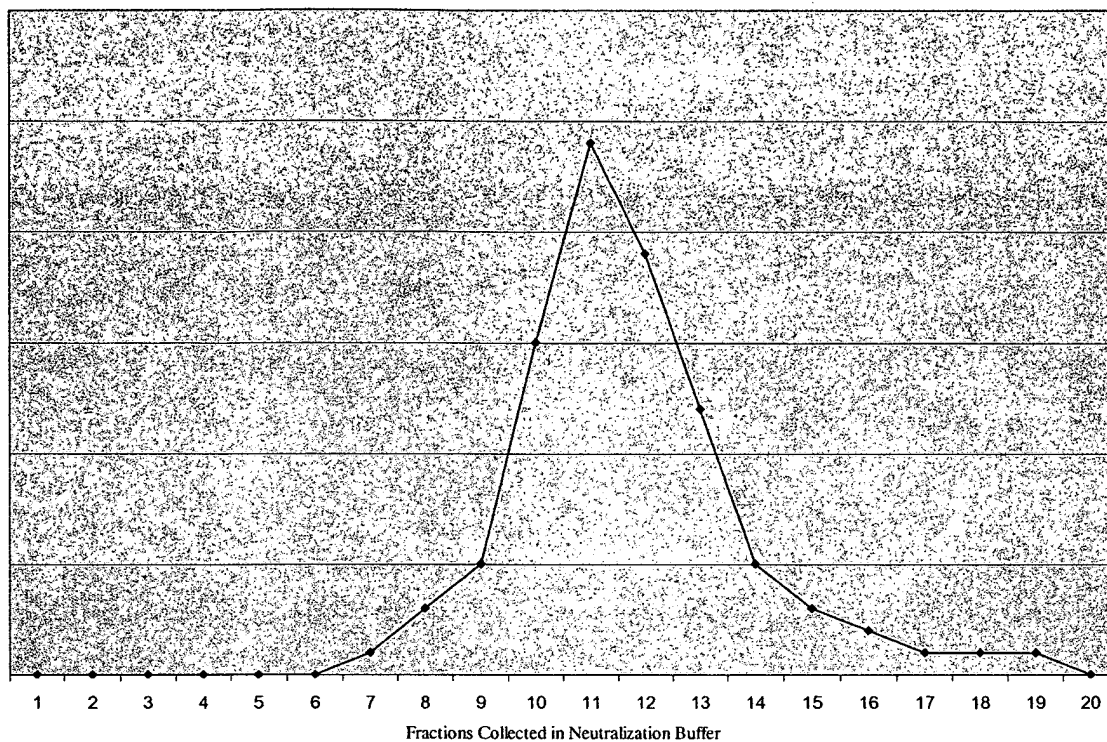


FIG. 45

ASSAY CONFIRMING BIOTINYLATION
Varying Reaction Times to Maximize Biotinylation Efficiency

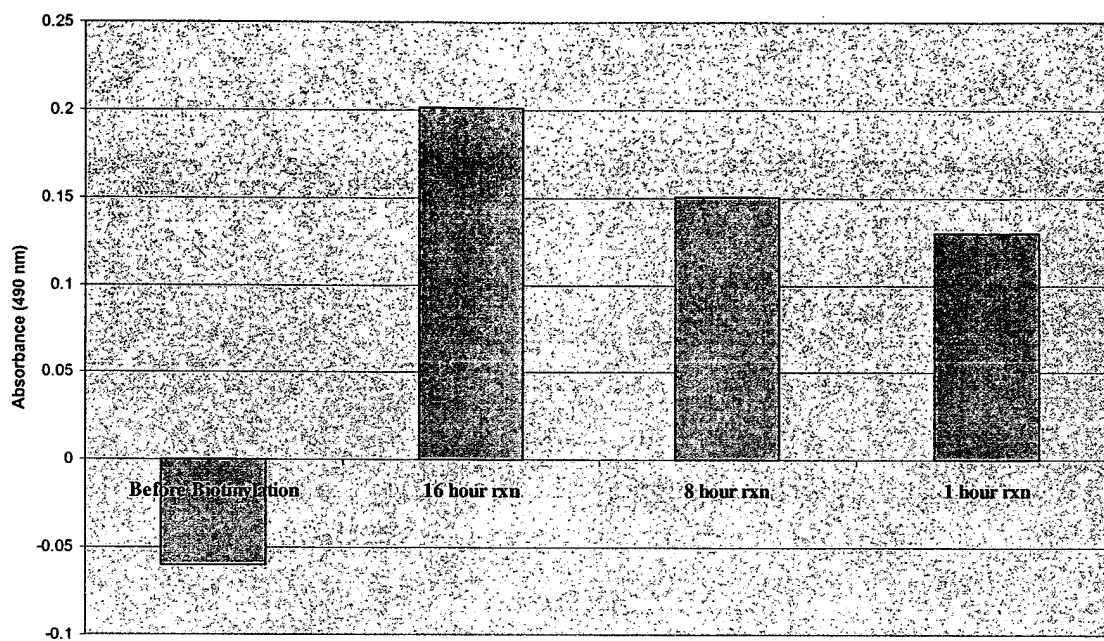


FIG. 46

SEPARATION OF BIOTINYLATED CLASS I FROM FREE BIOTIN

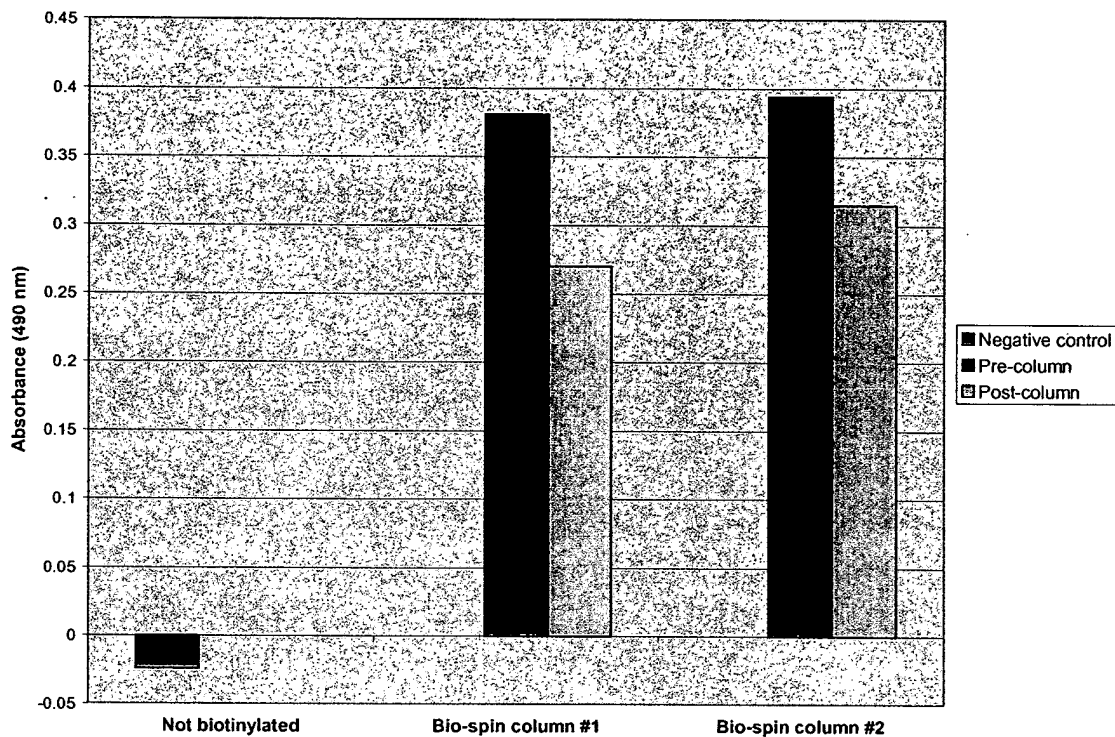


FIG. 47

	24	45	46	63	67	116	156	166	167	ethnicity
consensus	A	M	A	E	S	S	W	E	W	
B*1512	-	-	-	-	-	-	-	D	G	Thai
B*1508	-	-	-	N	F	-	-	-	-	Iranian/Indian/Amerindian
B*1501	-	-	-	-	-	-	-	-	-	Caucasian
B*1503	S	E	E	-	-	-	L	-	-	Black
B*1518	S	E	E	N	C	-	L	-	-	Indian
B*1510	S	E	E	N	C	Y	L	-	-	Black

TABLE 1

primer	type	sequence (5'→3')
HLA5UT	PCR (5'; inserts <i>SalI</i> site)	GGGCGTCGACGGACTCAGAAATCTCCCCAGACGCCGAG
sHLA3TM	PCR (3'; inserts stop codon and <i>HindIII</i> site)	CCGCAAGCTTT TCA TCTCAGGGTGAG
5PXI	PCR (5'; inserts <i>XbaI</i> site)	GGGCTCTAGAGGACTCAGAAATCTCCCCAGACGCCGAG
3PEI	PCR (3'; inserts stop codon and <i>EcoRI</i> site)	CCGCGAATTC TCA TCTCAGGGTGAG
M13 universal	sequencing (mp18, end through α_3) (mp19, leader through α_2)	TGTAAACGACGGCCAGT
3S	sequencing (α_2 through α_3)	CGGCAAGGATTACATCGCCCTG
JD3S	sequencing (α_3 through end)	CCCCATCGTGGGCATCGTTG
3N	sequencing (α_2 through leader)	CAGGGCGATGTAATCTTGCCG
4N	sequencing (α_3 through α_2)	GCCAGGTCAGTGTGATCTCCGC
T7 promoter	sequencing (T7 promoter forward priming site)	TAATACGACTCACATATAGGG
pcDNA3.1/BGH	sequencing (BGH reverse priming site)	TAGAAGGCACAGTCGAGG

TABLE 2

allele	# fractions	P2 extras	P9 extras	>9 cycles?
B*1501	7	P	-	yes (14)
B*1508	8	QVKRS	IVMQ	yes (14)
B*1503	3	P	MNL	yes (14)
B*1510	3	PR	MIY	yes (14)

TABLE 3

ligand	source protein	allele(s) characterized from
<i>HLA ligands</i>		
VGYVDDTQF	HLA-I α (49-57)	B*1501, 1508
IAVGYVDDTQF	HLA-I α (47-57)	B*1501, B*1512
IKADHVSTY	HLA-II DP α (32-40)	B*1503
GSHSMRYF	HLA-I α (25-32)	B*1503
<i>Replication/transcription/translation ligands</i>		
GQRKGAGSVF	60S ribosomal protein L8 (7-16)	B*1501, 1503
AQAESLRY	40S ribosomal protein S3 (100-107)	B*1501
GKVRTDITY	40S ribosomal protein S4 (73-81)	B*1503
SHAQTVVL	40S ribosomal protein S27 (48-55)	B*1510
SQFGGGSQY	eIF3-p66 (61-69)	B*1501, 1503, 1508, B*1512
VQGPVGTDF	zinc finger transcription factor (296-304)	B*1501
APPPPPPPP	transcription factor ZFM1 (581-589)	B*1501
YQHTGAVL	spleen mitotic checkpoint BUB3 (53-60)	B*1510
AHGRKMSKSL	valyl-tRNA synthetase (859-868)	B*1510
LPHQPLATY	Oct-binding factor 1 (52-60)	B*1508
AKYSTPATL	probable ATP-dependent RNA helicase DDX10 (280-288)	B*1503
AKAGITTTL	DNA replication licensing factor MCM5 (470-478)	B*1503
TQAPGNPVL	splicing factor U2AF large chain (179-187)	B*1510
SHQRQLLL	Kin17 (49-56)	B*1510
NQFQALLQY	polypyrimidine tract-binding protein (220-228)	B*1512
<i>Biosynthetic/degradative modification ligands</i>		
FVSNHAY	aldolase A (358-364)	B*1501, 1508
ILGPPGSVY	ubiquitin-protein ligase (83-91)	B*1501, B*1502, 1508, B*1512
YMIDPSGVSY	proteasome subunit C8 (150-159)	B*1501, B*1502, 1508, B*4601, B*1512
NHAIVSTSV	26S protease (S4) regulatory subunit (741-749)	B*1510
IHTPENPVI	lanosterol 14- α demethylase (488-496)	B*1510

TABLE 4

AHSNLASVL	O-linked GlcNAc transferase (237-245)	B*1510
Signalling/modulatory ligands		
VVAPITGY	calcyclin binding protein (63-71)	B*1501, 1508
GHSPPTSSL	tyrosine-protein kinase JAK3 (491-499)	B*1510
LPPPPPPPP	Fas antigen ligand (54-62)	B*1503
NHANGTL	serine/threonine protein phosphatase PP2A (α and β) (229-236)	B*1510
Transporter/chaperone ligands		
EHVASSPAL	13S Golgi transport complex 90 kD subunit (741-749)	B*1510
HHSDGSVSL	tapasin (354-362)	B*1509, B*1510
QPGPQIVY	GABA/noradrenaline transporter (261-268)	B*1503
Structural/cytokinesis ligands		
NMNDLVSEY	tubulin β chain (414-422)	B*1508
THTQPGVQL	sepin 2 homolog (70-78)	B*1509, B*1510
SHANSVVL	β -adaptin (249-257)	B*1509, B*1510
Unknown function ligands		
GQYPTQPTY	KIAA0058 (5-13); like <i>Mus musculus</i> proline-rich protein	B*1503
VKVIQGESY	mammary tumor-associated protein INT6 (278-286)	B*1503
AKYPHVEDY	Ki nuclear autoantigen (207-215)	B*1503
AMNPTNTVF	heat shock cognate 71 kD protein (60-68)	B*1503
CPLSCFT	human HTGS database	B*1501, B*1503, B*1508
MPHSGYGF	human EST	B*1508
CHSAFAL	human HTGS database	B*1510
LHLLTLEA	human EST	B*1510
KNANLVQLY	human EST	B*1512

TABLE 4 CONT'D.

fraction	ion for MS/MS	derived peptide sequence
7	504.1 (+2)	H M S G Z P T S Y
7	549.2 (+2)	H N Z A A H Z E Y
8	526.0 (+2)	H A A X Y S Z V Y
10	484.3 (+2)	Y Q S D H R Y
11	424.3 (+2)	H X S T Z D F
11	464.3 (+2)	H A P P T D P P P
11	550.0 (+2)	H G P A N R D S V F
11	563.3 (+2)	F P Y P T D P Z Y
12	531.2 (+2)	Z N A N X V Z X Y
14	585.6 (+2)	R S F X X E N E Y
16	488.7 (+2)	H M Z N P T S Y
16	661.9 (+2)	Y V X F - - - V Y
17	577.6 (+2)	R S M X R C P E Y
18	523.0 (+2)	- - F Y T A Z T Y
20	582.4 (+2)	M Y N C N E X D Y
25	562.8 (+2)	N Q F Q A L L Q Y

TABLE 5

Table 6

ALLELE	7	9	24	25	26	34	35	36	45	62	63	66	67	70	99	159	163	167	P2 MOTIF (dominant/str ong)
consensus	Y	Y	A	V	G	V	R	F	M	R	E	I	S	N	Y	Y	L	W	
B*1508	-	-	-	-	-	-	-	-	-	-	N	-	F	-	-	-	-	-	PA
B*1513	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	ILQVP
B*1502	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	LVQP
B*1501	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	QMLV
B*1512	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	QLM
B*1503	-	-	S	-	-	-	-	-	E	-	-	-	-	-	-	-	-	-	QKM
B*1518	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	H
B*1509	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	H
B*1510	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	H
B*1517	-	-	-	-	-	-	-	-	-	-	-	N	M	S	-	-	-	-	TS
B*1516	-	-	-	-	-	-	-	-	-	-	-	N	M	S	-	-	-	-	T
B*4601	-	-	-	-	-	-	-	-	-	-	-	K	Y	Q	-	-	-	-	MI

Table 6

ALLE LE	7 0	7 3	7 4	7 6	7 7	8 0	8 1	8 4	9 5	9 6	9 7	1 4	1 6	1 8	1 3	1 4	1 2	1 4	1 4	1 4	1 4	P9 MOTIF (dominan t/strong)	
<i>cons ensu s</i>	<i>N</i>	<i>T</i>	<i>Y</i>	<i>E</i>	<i>S</i>	<i>N</i>	<i>L</i>	<i>Y</i>	<i>L</i>	<i>Q</i>	<i>R</i>	<i>D</i>	<i>S</i>	<i>Y</i>	<i>Y</i>	<i>I</i>	<i>I</i>	<i>T</i>	<i>K</i>	<i>W</i>			
B*1 502	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	-	-	YFM	
B*1 501	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF	
B*1 503	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF	
B*1 508	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF	
B*1 512	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF	
B*1 518	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF	
B*4 601	Q	-	D	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF	
B*1 517	S	-	-	-	N	I	A	-	-	-	-	H	D	-	-	-	-	-	-	-	-	YF	
B*1 516	S	-	-	-	N	I	A	-	W	-	-	-	-	-	-	-	-	-	-	-	-	Y	
B*1 509	-	-	-	-	-	-	-	-	-	-	-	N	Y	-	-	-	-	-	-	-	-	LF	
B*1 510	-	-	-	-	-	-	-	-	-	-	-	-	Y	-	-	-	-	-	-	-	-	LF	
B*1 513	-	-	-	-	N	I	A	-	I	-	-	-	-	-	-	-	-	-	-	-	-	W	

TABLE 7

TABLE 7

fraction	ion for MS/MS	derived peptide sequence
9	490.3 (+2)	A G G Z P A T P P A X
9	513.1 (+2)	S H Z G C V Z P A V
10	433.8 (+2)	G H D P D S P A A
10	455.4 (+2)	E H V A S S P A L
10	482.6 (+2)	M C Z - G M P A X
10	482.8 (+2)	G H G A N N D P A X
10	495.7 (+2)	X H S Z P A G P A X
11	448.9 (+2)	M H A D N P V X
11	482.8 (+2)	G H <u>C</u> P R N P A X
11	495.7 (+2)	X H S G A P Z A P X
11	516.7 (+2)	X H D T <u>E</u> H A P X
12	448.4 (+2)	T Q A P G N P V L
12	460.3 (+2)	T Z A G <u>C</u> M V P X
13	464.8 (+2)	M V - - H P V X
14	456.7 (+2)	A H S V P S P A F
14	477.7 (+2)	M H T - - P A P V
14	482.8 (+2)	P G A A V V P S X
15	510.1 (+2)	I H T P E N P V I
16	456.7 (+2)	S H <u>D</u> G S V P T X
16	522.7 (+2)	- - - - - P V X
16	523.3 (+2)	M A H S - - P V F
17	523.2 (+2)	- H - - - - P V F
18	474.8 (+2)	M X <u>G</u> <u>X</u> S F P A X
18	491.2 (+2)	V H T C V N P V X
18	515.8 (+2)	E W <u>H</u> <u>Y</u> P V S X
19	496.6 (+2)	<u>E</u> T <u>P</u> <u>E</u> H A P V X

TABLE 8

side chain	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain
G	-	-	11.90%	10.32%	11.90%	-	-	-	G
P	-	10.32%	-	-	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	18.25%	11.11%	11.90%	-	-	-	10.32%	-	A
V	11.90%	-	-	-	-	10.32%	-	-	V
F	-	-	-	-	-	-	-	26.19%	F
M	-	-	-	-	-	-	-	-	M
I/L	13.49%	13.49%	-	-	-	-	-	-	I/L
S	-	-	-	-	-	-	-	-	S
T	-	-	-	-	-	13.49%	-	-	T
Y	-	-	-	-	-	-	-	63.49%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	24.60%	-	-	-	-	15.87%	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	10.32%	-	E
N value	13.64	19.52	3.80	0.32	1.90	3.81	6.51	69.68	C value
N _{sum}	37.28				81.90				C _{sum}
B*1501 N _{sum} /C _{sum} = 0.46									

TABLE 9

side chain	P1	P2	P3	P4	C ³	C ²	C ¹	C-t m	side chain
G	12.16%	-	12.16%	13.51%	12.16%	-	-	-	G
P	-	10.81%	-	12.16%	10.81%	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	31.08%	-	-	-	-	-	-	-	A
V	-	-	-	-	-	-	-	-	V
F	-	-	-	-	-	-	-	20.27%	F
M	-	-	-	-	-	-	-	-	M
I/L	-	-	-	-	-	13.51%	-	-	I/L
S	-	-	-	-	-	10.81%	-	-	S
T	-	-	-	-	-	13.51%	17.57%	-	T
Y	-	-	-	-	-	-	-	68.92%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	43.24%	-	-	13.51%	12.16%	14.86%	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	-	E
N value	23.24	34.05	2.16	5.67	6.48	9.99	12.43	69.19	C value
N _{sum}	65.12				98.09				C _{sum}
	B*1503 N _{sum} /C _{sum} = 0.66								

TABLE 10

side chain	P1	P2	P3	P4	C ¹	C ²	C ³	C ⁴	C-term	side chain
G	-	-	-	-	-	-	10.42%	-	-	G
P	-	27.08%	-	-	-	-	-	-	-	P
C	-	-	-	-	-	-	-	-	-	C
A	-	16.67%	13.54%	-	-	-	-	14.58%	-	A
V	-	-	-	-	-	11.46%	-	12.50%	-	V
F	-	-	-	-	-	-	-	-	23.96%	F
M	-	-	-	-	-	-	-	-	-	M
I/L	11.46%	-	-	-	-	-	-	-	-	I/L
S	-	-	-	-	-	11.46%	-	11.46%	-	S
T	10.42%	-	-	-	-	-	-	17.71%	-	T
Y	11.46%	-	-	-	-	-	-	-	66.67%	Y
N	-	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	-	W
Q/K	-	-	-	-	-	-	12.50%	-	-	Q/K
H	-	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	10.42%	-	E
N value	3.34	23.75	3.54	0.00	2.92	2.92	16.67	70.63	C value	
N _{sum}	30.63				93.14				C _{sum}	
B*1508 N _{sum} /C _{sum} = 0.33										

TABLE 11

side chain	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain
G	10.57%	-	10.57%	10.57%	-	-	11.38%	-	G
P	-	-	-	12.20%	-	28.46%	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	-	19.51%	-	-	-	14.63%	-	A
V	-	-	-	-	-	-	22.76%	10.57%	V
F	-	-	-	-	-	-	-	-	F
M	11.38%	-	-	-	-	-	-	-	M
I/L	12.20%	-	-	-	-	-	12.20%	70.73%	I/L
S	11.38%	-	-	-	-	-	15.45%	-	S
T	-	-	-	-	-	-	-	-	T
Y	-	-	-	-	-	-	-	-	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	-	-	-	-	-	-	-	Q/K
H	-	58.54%	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	-	E
N value	5.53	48.54	10.08	2.77	1.38	18.46	25.04	61.3	C value
N _{sum}	66.92				106.18				C _{sum}
B*1510 N _{sum} /C _{sum} = 0.63									

TABLE 12

side chain	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain
G	-	-	-	-	-	-	-	-	G
P	-	-	-	13.33%	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	16.67%	-	13.33%	-	-	-	-	A
V	-	-	-	-	16.67%	-	-	-	V
F	-	-	16.67%	-	-	-	-	16.67%	F
M	-	13.33%	-	-	-	-	-	-	M
I/L	-	13.33%	13.33%	16.67%	-	-	-	-	I/L
S	-	-	-	-	13.33%	-	-	-	S
T	-	-	-	-	13.33%	-	-	-	T
Y	13.33%	-	-	-	-	-	-	80.00%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	16.67%	13.33%	-	20.00%	13.33%	-	-	Q/K
H	23.33%	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	13.33%	16.67%	-	-	-	D
E	-	-	-	-	-	-	16.67%	-	E
N value	16.66	20.00	13.33	16.66	6.67	16.66	16.67	76.67	C value
N _{sum}	66.65				116.67				C _{sum}
B*1512 N _{sum} /C _{sum} = 0.57									

TABLE 13

fraction	ion for MS/MS	derived peptide sequence	alleles overlapping
6	398.2 (+3)	- - W D R H T X F	B*1501/B*1508
6	448.2 (+2)	- - - - - Y T	B*1501/B*1508
7	418.7 (+2)	A Q F A S G A G Z	B*1501/B*1503
8	402.2 (+2)	- G - - C D Y	B*1501/B*1503
8	418.7 (+2)	G S H F G V A Y	B*1501/B*1508
8	516.7 (+2)	N Q Z H G S A E Y	B*1501/B*1503/B*1508/B*1512
8	642.7 (+2)	P M N D W X M T Z T Y	B*1501/B*1512
9	331.4 (+3)	A P M A R G Z Y	B*1501/B*1503
9	418.7 (+2)	F V S N H A Y	B*1501/B*1508
9	433.2 (+2)	N P P A Z Z P N	B*1501/B*1503
9	437.0 (+2)	T G - - - - A Y	B*1501/B*1508
9	441.2 (+2)	- Q - D P P P D M Z Y	B*1501/B*1503
9	446.6 (+2)	G Q Z Z A V D F	B*1501/B*1503
9/10	465.2 (+2)	S Q F G G G S Q Y	B*1501/B*1503/B*1508/B*1512
9	476.2 (+2)	S Q F D H V T Y	B*1501/B*1508
9	578.0 (+2)	T P X G E P Y Z S Y	B*1501/B*1503/B*1508
10	398.3 (+2)	X A N - - V T	B*1501/B*1508
10	456.8 (+2)	C P L S C F T	B*1501/B*1503/B*1508
10	509.0 (+2)	F L Z A M Z S T Y	B*1501/B*1508/B*1512
10	532.0 (+2)	T V X D S Z T H Y	B*1501/B*1508/B*1512
13	503.6 (+2)	G Q R K G A G S V F	B*1501/B*1503
14	460.7 (+2)	V V A P I T T G Y	B*1501/B*1508
14	475.1 (+2)	V V A C V - - - Y	B*1501/B*1508
14	525.3 (+2)	P L A - N - H T Y	B*1501/B*1508
15	514.2 (+2)	F Q A R X T E Y	B*1501/B*1508
16	522.0 (+2)	V G Y V D D T Q F	B*1501/B*1508
17	351.3 (+3)	A A F C G - - - X V	B*1501/B*1508
17	408.7 (+2)	Y L H - - E T	B*1501/B*1508
17/18	451.4 (+2)	I L G P P G S V Y	B*1501/B*1508/B*1512
17	462.4 (+2)	X L G D V N M Y	B*1501/B*1508
17	507.0 (+2)	- - - - X V E F	B*1501/B*1508
17	519.2 (+2)	T A R V X S V E Y	B*1501/B*1508
18	565.7 (+2)	A E F W A C Z X Y	B*1501/B*1503
18/19	566.2 (+2)	Y M I D P S G V S Y	B*1501/B*1508/B*1512
19/20	560.0 (+2)	X V E X T T D Y Y	B*1501/B*1512
20/21	448.2 (+2)	A A G X G P T F Y	B*1501/B*1512
20/21	614.0 (+2)	I A V G Y V D D T Q F	B*1501/B*1512
21/22	507.2 (+2)	V A F V X F V G Y	B*1501/B*1512
21/22	557.2 (+2)	Y N R W S X E F	B*1501/B*1512
22/23	510.8 (+2)	A L M P - - X N Y	B*1501/B*1512

TABLE 14

allele	ion overlaps collided	positive overlaps	overlap frequency
B*1512	20	14	70%
B*1508	286	25	9%
B*1503	88	12	14%
B*1510	26	0	0%

TABLE 15

motif P2/P9		+ length variation only		+ P2 variation only	
DLASMLNRY	(64-72)	MQLLCVF	(1-7)	DIEGHASHY	(28-36)
MLNRYKLIY	(68-76)	HLDIEGHASHY	(26-36)	SAPLEKQLF	(123-131)
PLEKQLFYY	(125-133)	MLSAPLEKQLF	(121-131)	APLEKQLFY	(124-132)
YQLRCHLSY	(149-157)	PLEKQLF	(125-131)	LPNTRPHSY	(138-146)
ALSINGDKF	(159-167)	PLEKQLFY	(125-132)	NTRPHSYVF	(140-148)
DLPDLRGPF	(203-211)	TMLPNTRPHSY	(136-146)	SINGDKFQY	(161-169)
FVPNLKDMF	(242-250)	MLPNTRPHSY	(137-146)	YTGAMTSKF	(169-177)
AVTMTAASY	(253-261)	QLRCHLSY	(150-157)	TSKFLMGTY	(174-182)
TMFEVSVAF	(290-298)	YVALSINGDKF	(157-167)	L TSAQSGDY	(216-224)
DLRWLAKSF	(314-322)	FQYTGAMTSKF	(167-177)	YSLVIVTTF	(224-232)
HLTTEKQEY	(366-374)	AMTSKFLMGTY	(172-182)	VIVTTFVHY	(227-235)
ALRLATVGY	(375-383)	HVLSLVF	(192-198)	TTFVHYANF	(238-246)
ALGTESGLF	(467-475)	SLTSAQSGDY	(215-224)	MTAASYARY	(256-264)
AVSNAVDGF	(505-513)	SLVIVTTF	(225-232)	DTETLTTFM	(284-292)
ALYEASTTY	(564-572)	LVIVTTF	(226-232)	ATVKGMQSY	(338-346)
RQIPKIQNF	(597-605)	IVTTFVHY	(228-235)	ATSVLLSAY	(396-404)
ILSSNYFDF	(643-651)	IVTTFVHYANF	(228-238)	SAYNRHPLF	(402-410)
TVMEIAGLY	(666-674)	FVHYANFHNF	(232-241)	HTVMRETLF	(414-422)
HVVLAILLY	(679-687)	FVHYANFHNFY	(232-242)	ESGLFSPCY	(471-479)
VVLAILLYF	(680-688)	TMTAASY	(255-261)	SPCYLSLRF	(476-484)
FLVHKIVMF	(696-704)	TMTAASYARY	(255-264)	I IPLINVTF	(544-552)
LVHKIVMFF	(697-705)	ELDTETLTTFM	(282-292)	TTYLSSSLF	(570-578)
		TMFEVSVAFF	(290-399)	NSILSSNYF	(641-649)
		TVLKDIIGICY	(326-326)	AIILYFIAF	(683-691)
		VLKDIIGICY	(327-326)	FIAFALGIF	(688-696)
		TVKGMQSY	(339-346)		
		RLATVGY	(377-383)		
		TVGYPKAGVY	(380-389)		
		LLSAYNRHPLF	(400-410)		
		PLHTVMRETLF	(412-422)		
		VMRETLF	(416-422)		
		GLALGTESGLF	(465-475)		
		GLFSPCY	(473-479)		
		LMIIPLINVTF	(542-552)		
		PLINVTF	(546-552)		
		EVRGSAFY	(559-566)		
		YLSSSLF	(572-578)		
		TQKSCIF	(608-614)		
		TQKSCIFCGF	(608-617)		
		GLETTY	(627-633)		
		VQNSILSSNY	(639-648)		
		VQNSILSSNYF	(639-649)		
		ILSSNYF	(643-649)		
		VMEIAGLY	(667-674)		
		VVLAILLY	(680-687)		
		VVLAILLYF	(680-688)		
		VLAILLY	(681-687)		
		VLAILLYF	(681-688)		
		VLAILLYFIAF	(681-691)		
		ILYFIAF	(685-691)		
		FLVHKIVMFF	(696-705)		

TABLE 16

TABLE 17

Primer name	Sequence 5'-3'	Locus	Cut site	Annealing site
PP5UTA	GCGCTCTAGACCCAGACGCCGAGGATGGCC	A	XbaI	5UT
3PPI4A	GCCCTGACCCCTGCTAAAGGT	A		Intron 4
PP5UTB	GCGCTCTAGACCCACCCGGACTCAGAATCTCCT	B	XbaI	5UT
3PPI4B	TGCTTTCCTTGAGAAAGAT	B		Intron 4
5UTB39	AGCGGAATTCAGAGTCTCCTCAGACGCG	B*39	EcoRI	5UT B39
5PKCE	GGCGGAATTCGCCGCCACCATGCGGGTCATGGCGCC	C	EcoRI	5UT
3PPI4C	TTCTGCTTTCCTGAGAAAGAC	C		Intron 4
PP5UT	GGCGGAATTCGGACTCAGAACTCTCCCCAGACGCCGAG	B	EcoRI	5UT
PP3PEI	CCGCGAATTCATCTCAGGGTGAGGGGCT	A,B,C	EcoRI	Exon 4
PP3PEIH	CCGCAAGCTTTCATCTCAGGGTGAGGGGCT	A,B,C	HindIII	Exon 4
3PEIHC7	CCGCAAGCTTTCAGCTCAGGGTGAGGGGCT	Cw*07	HindIII	Exon 4

Primer Name	Sequence 5'-3'
T7Prom	TAATACGACTCACTATAGGG
BGHrev	TAGAAGGCACAGTCGAGG
PPI2E2R	GTCGTGACCTGCGCCCC
PPI2E2F	TTTCATTTTCAGTTTAGGCCA
ABCI3E4F	GGTGTCTCTGTCCATTCTCA

5'CY5 Sequencing Primers

TABLE 18

40022066-404004

TABLE 19

Sample	OD 260nm	OD 280nm	260nm/280nm	Dilution factor	Concentration ug/ml
3A394	0.0346	0.0202	1.7111	20	34.5821

for 90000

TABLE 20

Sample	OD 260nm	OD 280nm	260nm/280nm	Dilution factor	Concentration ug/ml
3A394TPC 1	0.2821	0.1505	1.8739	20	282.0960

2023-03-27 10:00:00

TABLE 21

Sample	OD 260nm	OD 280nm	260nm/280nm	Dilution factor	Concentration ug/ml
3A394TPC 1	0.6919	0.3625	1.9087	50	1729.8492

10022055-1004
10022055-1004

TABLE 22

Sample	Decay time milliseconds	# live cells/ml	# dead cells/ml	Viability %
3A394TPC 1	19.8	1.12×10^6	1.65×10^5	87.16

Downloaded from www.ascelibrary.org

TABLE 23

Sample	Optical Density 492nm	Dilution	Concentration of soluble HLA ng/ml
3A394TP C1 well 1	1.278 1.388 (over range)	1.0	247.270
3A394TP C1 well 2	1.227 1.274	1.0	229.855
3A394TP C1 well 3	1.021 1.042	1.0	154.403
3A394TP C1 well 4	1.108 1.070	1.0	169.001

TABLE 24

Allele	Allele Allele AlleleConcentration by ELISA ug/ml	Concentration by ELISA ug/ml Concentration by ELISA ug/ml Concentration by ELISA ug/mlTotal amount made mg
<u>Total amount made mg</u> <u>Total amount made mg</u> <u>Total amount made mg</u> <u>Total amount made mg</u> HLA- A*0301	545.4	3.47
HLA-A*1102	888.5	2.57
HLA-A*2902	476.8	2.58
HLA-A*3002	50.3	3.38
HLA-A*3201	1382.0	9.61
HLA-A*3301	40.0	0.8
HLA-B*0801	66.0	21.0
HLA-B*1302	55.0	9.0
HLA-B*1401	146.0	50.0
HLA-B*1801	587.6	0.4
HLA-B*3701	1831.0	119.0
HLA-B*3801	128.0	66.0
HLA-B*3905	1400.0	120.0
HLA-B*40012	59.0	10.0
HLA-B*4002	400.0	180.0
HLA-B*4101	288.4	8.8
HLA-B*4402	59.0	10.0

101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200

fraction	ion for MS/MS	derived peptide sequence
6	398.2 (+3)	- - W D R H T X F
6	448.2 (+2)	- - - - - Y T
7	382.7 (+2)	V Q F E A A T
7	418.7 (+2)	A Q F A S G A G Z
7	455.2 (+2)	A L G A - - R G Y
7	489.1 (+2)	- - V - - G H X Y
7	506.8 (+2)	X S - - - C E Y
8	402.2 (+2)	- G - - C D Y
8	419.2 (+2)	G S H F G V A Y
8	433.8 (+2)	A P P P P P P P P
8	455.2 (+2)	- - - Z A R G Y
8	462.2 (+2)	D P <u>H</u> <u>A</u> <u>P</u> Z Y
8	507.2 (+2)	A V P S X H X X Y
8	512.3 (+2)	X A Z V Z M T A Y
8	512.8 (+2)	A L N G R <u>V</u> <u>T</u> M Y
8	516.9 (+2)	N Q Z H G S A E Y
8	522.9 (+2)	F G <u>X</u> <u>A</u> <u>C</u> X A T S Y
8	642.7 (+2)	P M N D W X M T Z T Y
9	331.4 (+3)	A P M A R G Z Y
9	418.7 (+2)	F V S N H A Y
9	426.2 (+3)	- - - - - - - - S Y
9	433.3 (+2)	N P P A Z Z P N
9	437.0 (+2)	T G - - - - A Y
9	441.2 (+3)	- Q - D P P P D M Z Y
9	446.6 (+2)	G Q Z Z A V D F
9	453.6 (+2)	X Q - - A G G Z Y
9	465.2 (+2)	S Q F G G G S Q Y
9	476.2 (+2)	S Q F D H V T Y
9	481.0 (+2)	G Q H A S V X S Y
9	514.2 (+2)	- - A A H V P P G Y
9	550.2 (+2)	F M D V G A P T V Y
9	578.0 (+2)	T P X G E P Y Z S Y
10	398.3 (+2)	X A N - - V T
10	448.2 (+2)	A Q A A P F A G Y
10	448.4 (+2)	V V V F G V Z F
10	450.4 (+2)	A Q M - - S E Y
10	456.8 (+2)	C P L S C F T
10	464.7 (+2)	- - - - F G H Y
10	473.7 (+2)	<u>A</u> <u>L</u> W - - P Z F
10	486.4 (+2)	V P H Z N A Y

TABLE A CONT'D.

TABLE A - 9300000

10	498.7 (+2)	- - - - - G H G G Y
10	509.0 (+2)	F L Z A M Z S T Y
10	527.7 (+2)	G Q Y V V Z P T Y
10	532.0 (+2)	T V X D S Z T H Y
10	540.2 (+2)	P M F D P P Z T F
11	469.2 (+2)	A Q A E S L R Y
11	480.6 (+2)	X A V G H S G G T Y
11	511.2 (+2)	- - - - - P T Y
11	516.7 (+2)	E S X P N N V P Y
12	383.0 (+3)	L A H T E C P R G Y
12	435.0 (+2)	- - - - - P S Y
12	473.2 (+2)	V Q G P V G V Q Y
12	475.0 (+2)	R G X G V A G T A F
12	505.0 (+2)	T G A P V S E E G Y
12	513.7 (+2)	V Q X Y Y G S V V
12	519.0 (+2)	E P A M V X Z C F
12	531.2 (+2)	G Q P G A P X G G Z Y
12	541.0 (+2)	G P P H N G X R A Y
12	542.2 (+2)	A A H W H V E A Y
12	553.7 (+2)	T P P T R R E S Y
12	577.2 (+2)	F P T D R R S Q F
13	363.0 (+3)	Y T G V S Y X H F
13	447.0 (+2)	A Q A S A P D A Y
13	465.0 (+2)	V Q Y Y X P F
13	503.6 (+2)	G Q R K G A G S V F
13	553.2 (+2)	X Q Z X - - D V Y
13	590.8 (+2)	A T G T A Z N X N Z Y
14	460.7 (+2)	V V A P I T T G Y
14	471.5 (+2)	V V A C V - - - Y
14	495.2 (+2)	X Q Y T V G Y F
14	525.3 (+2)	P L A - N - H T Y
14	541.3 (+2)	P L F G Q T A G Q Y
14	550.4 (+2)	A - - - - Q X E Y
14	577.2 (+2)	Z G Y G N P X N G A Y
15	459.8 (+2)	V Q G P V G T D F
15	470.9 (+2)	V A G G W - - - F
15	514.2 (+2)	F Q A R X T E Y
15	536.6 (+2)	X A G F F X X E Y
15	544.2 (+2)	X Q - - - - Z Y
15	564.2 (+2)	S G A X D R A Y Z F
16	467.1 (+2)	F Q - - - - T X
16	500.4 (+2)	T P - - - A Z A F
16	501.0 (+2)	V V A T Z N Z Z X
16	503.6 (+2)	Y M V T - - - F
16	517.4 (+2)	A L G S Z A X M P F
16	521.3 (+2)	A P A V - - - V G Y
16	522.0 (+2)	V G Y V D D T Q F
16	525.6 (+2)	- - - - - T G F

TABLE A CONT'D.

16	536.0 (+2)	P V P N V R X N Y
16	544.4 (+2)	- - - - - T X S X
16	557.6 (+2)	T L E G W M S Z Y
16	561.5 (+2)	Y M V C N A E E Y
16	596.7 (+2)	- - - - - X R D X Y
16	596.9 (+2)	S L X - - - - F
17	343.2 (+3)	A Q H P <u>S</u> <u>A</u> <u>X</u> R F
17	351.3 (+3)	A A F C G - - - X V
17	408.7 (+2)	Y L H - - E T
17	441.2 (+2)	- - - - - Z A Y
17	451.4 (+2)	I L G P P G S V Y
17	455.0 (+2)	G L G Z T S A E F
17	462.4 (+2)	X L G D V N M Y
17	483.8 (+2)	V M <u>G</u> <u>X</u> <u>T</u> <u>N</u> A N F
17	490.2 (+2)	N A X G R E S S F
17	497.2 (+2)	A M N P T N T V F
17	507.0 (+2)	- - - - X V E F
17	511.2 (+2)	X Q A P A X F V Y
17	519.2 (+2)	T A R V X S V E Y
17	526.8 (+2)	A L F - - - F T Y
17	542.8 (+2)	X Q X N A Y X S Y
17	563.2 (+2)	G L A R C <u>S</u> Z V E Y
18	503.8 (+2)	S Q X <u>A</u> <u>A</u> <u>G</u> V D V F
18	511.7 (+2)	P Q G Z M A - - Y
18	519.6 (+2)	- V F V S H T T F
18	538.8 (+2)	<u>H</u> X T G <u>N</u> E A T S F
18	565.7 (+2)	A E <u>F</u> <u>W</u> A C Z X Y
18	566.2 (+2)	Y M I D P S G V S Y
18	581.2 (+2)	X Q G H H E M F Y
20	448.2 (+2)	A A G X G P T F Y
20	560.0 (+2)	X V E X T T D Y Y
20	614.0 (+2)	I A V G Y V D D T Q F
21	507.2 (+2)	V A <u>F</u> <u>V</u> <u>X</u> F V G Y
22	510.8 (+2)	<u>A</u> <u>L</u> M P - - X N Y
22	557.2 (+2)	Y N <u>R</u> <u>W</u> S X E F
24	546.3 (+2)	- - Z D R N V T F
25	546.3 (+2)	V V T M - - - Z Y

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

TABLE B

fraction	ion for MS/MS	derived peptide sequence
6	471.8 (+2)	A Z V E C E T Y
7	418.7 (+2)	A Q F A S G A G Z
7	504.2 (+2)	Z G X G G G P A T S Y
8	402.2 (+2)	- G - - C D Y
8	441.2 (+2)	- - - - - Z S F
8	516.9 (+2)	N Q Z H G S A E Y
9	331.4 (+3)	A P M A R G Z Y
9	349.4 (+3)	- - - - - G F Y
9	418.7 (+2)	A Z V N S G - Y
9	426.2 (+3)	A A S S Z V - - P P Z Y
9	433.3 (+2)	N P P A Z Z P N
9	437.0 (+2)	A C G G C G Z D Y
9	441.2 (+3)	- Z - D P P P D M Z Y
9	446.6 (+2)	G Q Z Z A V D F
9	578.0 (+2)	T P X G E P Y Z S Y
10	426.5 (+2)	G P - - - P Z Y
10	443.2 (+2)	A P Z Y P P P P
10	448.3 (+2)	G Z V C T P G S F
10	456.8 (+2)	C P L S C F T
10	464.7 (+2)	S Q F G G G S Q Y
10	465.4 (+2)	A S G F N G S Z Y
10	503.8 (+2)	- Z - - Y T A Y
10	508.7 (+2)	G Z P P H N G F Y
10	517.0 (+2)	I K A D H V S T Y
10	527.7 (+2)	X Z A D H V X P Y
10	540.2 (+2)	- - - - P G Z V Y
10	549.2 (+2)	Z S V - - - Z T G Y
11	437.0 (+2)	H X G N Q A A Y
11	511.4 (+2)	Z A G T T V P V S Y
11	527.4 (+2)	G Q Y P T Q P T Y
11	581.4 (+2)	F A G S Z S N T S T Y
12	494.8 (+2)	S Z G G - - - T G Y
12	526.8 (+2)	Z G P P N Y X T Y
12	547.1 (+2)	V K V I Q Q E S Y
13	454.6 (+2)	L P P P P P P P P
13	476.0 (+2)	A K Y S T P A T L
13	503.6 (+2)	G Q R K G A G S V F
13	513.1 (+2)	R Z S A N H E A X
13	526.4 (+2)	G K V R T D I T Y
13	553.2 (+2)	V V X P A V R S T Y

10022066-434004

**TABLE B
CONT'D.**

13	561.0 (+2)	A K Y P H V E D Y
13	571.3 (+2)	A Z N X S A Y V X Y
13	601.2 (+2)	E V V G D T Z Y
14	438.2 (+2)	A K A G I T T T L
14	490.8 (+2)	V - - T Z A G S A F
14	517.2 (+2)	A Z A A A N V X X Y
14	531.5 (+2)	A N H S V R D T Y
14	535.3 (+2)	E - - - G X R Z Y
14	552.8 (+2)	X Z H N D Z S T Y
14	577.2 (+2)	A N E Z X G - - - Y
15	497.3 (+2)	A A G P T A Z E S Y
15	514.2 (+2)	V A G X V F M Z Y
15	527.0 (+2)	A Z Y Z A Z V V F
15	564.2 (+2)	A Z F - - - Z X Y
15	577.2 (+2)	Z G Y G N P X N Z Y
15	626.0 (+2)	- - - - - Z A P C H Y
16	521.6 (+2)	A H A V Q R V V Y
16	525.6 (+2)	T Z X T V V X N Y
17	446.8 (+2)	A Z Z A S G X A F
17	492.8 (+2)	G S H S M R Y F
17	503.8 (+2)	Y G Y G A T V E F
17	967.6 (+1)	V Z - - - T T F
18	451.4 (+2)	Q P G P Q I V Y
18	455.2 (+2)	N G Z X S N N Y
18	475.2 (+2)	A N X V Z X E Y
18	489.1 (+2)	G Z - - - Z G X X Y
18	497.8 (+2)	A M N P T N T V F
18	525.2 (+2)	Y N - - - Z X F
18	538.8 (+2)	- M - - S Y Z N F
18	565.7 (+2)	A E <u>F</u> W A C Z X Y
19	521.6 (+2)	S Z F G <u>C</u> <u>P</u> T R F
19	524.6 (+2)	X G A X S N - - E F
19	571.2 (+2)	R Z A A Y R X T Y
19	646.2 (+2)	T N X H D G D G A T Z Y

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

4003162-4003164

TABLE C

fraction	ion for MS/MS	derived peptide sequence
6	398.2 (+3)	- - W D R H T X F
6	448.2 (+2)	- - - - - Y T
8	419.2 (+2)	G S H F G V A Y
8	441.2 (+2)	V P C G Z Z S Y
8	473.2 (+2)	T A Z X H R G Y
8	512.8 (+2)	X A Z Y E H T Y
8	516.9 (+2)	N Q Z H G S A E Y
8	546.8 (+2)	N G X A M H W T Y
9	418.7 (+2)	F V S N H A Y
9	437.0 (+2)	T G - - - - A Y
9	465.2 (+2)	S Q F G G G S Q Y
9	476.2 (+2)	S Q F D H V T Y
9	481.0 (+2)	- P - - G Z D E V
9	514.2 (+2)	N G Y D G P N A G Y
9	578.0 (+2)	T P X G E P Y Z S Y
10	398.3 (+2)	X A N - - V T
10	448.3 (+2)	M P H S G Y G F
10	450.4 (+2)	V D X - - - Y
10	456.8 (+2)	C P L S C F T
10	464.7 (+2)	- - - - - P G F Y
10	486.2 (+2)	- A - P H P M G Y
10	494.2 (+2)	A Q T V G Y G E Y
10	508.7 (+2)	- - - - - S V Y
10	509.0 (+2)	F L Z A M Z S T Y
10	532.0 (+2)	T V X D S Z T H Y
11	444.1 (+2)	T P - - A R A P T
11	469.2 (+2)	S E H D R M Y
11	480.6 (+2)	T G N C S G T G T Y
11	496.8 (+2)	A Q V N P S X T Y
11	532.3 (+2)	S P G A E T R A X Y
12	473.2 (+2)	Y L G - - - G A F
12	494.8 (+2)	X T S F M Z V Y
12	499.0 (+2)	- P - - - P S S G Y
12	505.0 (+2)	T P - - - G R M Y
12	513.7 (+2)	P M F D Z Z V Y
12	519.0 (+2)	Y L - - - R T F
12	531.2 (+2)	A Q E H G C A A Z F
12	542.2 (+2)	- M - - - G Y H D Y
12	550.2 (+2)	Y V S - - R N Q Y
12	553.7 (+2)	A Q Y A A G E S F Y

TABLE C

TABLE C
CONT'D.

12	564.0 (+2)	T P H T Z H D E Y
12	565.2 (+2)	Y M - - - F M Y
13	396.1 (+3)	D P H Y V S G H Z F
13	401.2 (+2)	M V G X X P A T
13	526.4 (+2)	Z A S P G E X T S Y
14	460.7 (+2)	V V A P I T T G Y
14	471.5 (+2)	V V A C V - - - Y
14	525.3 (+2)	P L A - N - H T Y
14	543.2 (+2)	X A X Y R R M Y
14	550.4 (+2)	P L A M Z X Y T Y
15	460.6 (+2)	- P - M P G X A Y
15	461.0 (+2)	H T T S Z N A Y
15	506.0 (+2)	M A A M V G V A V Y
15	508.4 (+2)	G P Z V M Z H G Y
15	514.2 (+2)	F Q A R X T E Y
15	520.0 (+2)	L P H Q P L A T Y
15	525.2 (+2)	A A A X V - - - V T Y
15	536.6 (+2)	X P E M G Z F S Y
15	544.2 (+2)	Y V - - V R - V F
15	564.2 (+2)	F V T X N X E E Y
16	489.0 (+2)	A A P V G A X E S Y
16	500.4 (+2)	G S - - - S Y T Y
16	522.0 (+2)	V G Y V D D T Q F
16	525.7 (+2)	Y V A - - - P A F
16	533.0 (+2)	V G Y - - A H P G F
16	535.7 (+2)	Z A T N S V T S T Y
16	537.0 (+2)	- - - - - S T Y
16	545.8 (+2)	Y A T A G E M M A F
16	547.0 (+2)	S P T Y T H A V A F
16	557.0 (+2)	M P A - - M V M A F
17	351.3 (+3)	A A F C G - - - X V
17	393.7 (+2)	S P N E D X M Z V F
17	403.2 (+2)	V A A T A G A V F
17	408.7 (+2)	Y L H - - E T
17	414.8 (+2)	T A F P F V F
17	451.4 (+2)	I L G P P G S V Y
17	462.4 (+2)	X L G D V N M Y
17	476.2 (+2)	Y G - - - V X S M
17	490.8 (+2)	X P H C S C S S F
17	504.0 (+2)	D P P C W G V S F
17	507.0 (+2)	- - - - X V E F
17	511.2 (+2)	- - - - A H D A Y
17	519.2 (+2)	T A R V X S V E Y
17	526.8 (+2)	X S D G R Z X T Y
17	542.8 (+2)	N M N D L V S E Y
17	557.2 (+2)	M P A A D Y E V A F
18	474.8 (+2)	A E I L Q V I Y
18	503.8 (+2)	A P - - - X V S Y

1002055 1004004

TABLE D
CONT'D.

11	405.7 (+2)	S H - - - Y F
11	425.8 (+2)	A H P D Z A X V
11	444.7 (+2)	G T A H Y Z V X
11	448.9 (+2)	M H A D N P V X
11	455.7 (+2)	S H <u>V</u> <u>D</u> R P S X
11	459.7 (+2)	T G A A F Z N P X
11	482.8 (+2)	G H <u>C</u> <u>P</u> R N P A X
11	495.7 (+2)	X H S G A P Z A P X
11	516.7 (+2)	X H D <u>T</u> <u>E</u> H A P X
11	562.3 (+2)	- - - Y Z A Y V Y
12	411.7 (+2)	G H G P T X A A V
12	428.8 (+2)	V P - - - - -
12	444.7 (+2)	Y Q H T G A V L
12	448.4 (+2)	T Q A P G N P V L
12	460.3 (+2)	T Z A <u>G</u> <u>C</u> <u>M</u> <u>V</u> P X
12	490.9 (+2)	T H T Q P G V Q L
12	507.4 (+2)	G H A G H V P P E X
12	511.6 (+2)	T H F R Y V S X
12	528.1 (+2)	E H R P D R V F
13	427.6 (+2)	S H A Q T V V L
13	449.2 (+2)	S H A N S A V V L
13	464.8 (+2)	M V - - H P V X
13	487.6 (+2)	Y H H G G V S A F
13	506.2 (+2)	- H - - G H T G Y X
14	420.1 (+2)	N H A N G L T L
14	438.7 (+2)	- - - - - P X X
14	456.7 (+2)	A H S V P S P A F
14	477.7 (+2)	M H T - - P A P V
14	482.8 (+2)	P G A A V V P S X
14	560.8 (+2)	G H A G M G C V F Z X
14	592.3 (+2)	M R - - - - G X E X
15	418.9 (+2)	S H G V P R A X
15	439.0 (+2)	E H H M P X X
15	454.3 (+2)	H H Z C A A G A X
15	492.1 (+2)	X V D <u>Z</u> A <u>E</u> P X V
15	510.1 (+2)	I H T P E N P V I
15	520.0 (+2)	M G X P V R H M V
15	524.2 (+2)	S H Y D W Z V X
15	532.9 (+2)	M P H S H P F V X
15	577.2 (+2)	Z C V R C Z N G V F
16	412.9 (+2)	S H A G A G X V X
16	418.3 (+2)	G H X E G P X X
16	424.3 (+2)	X H G G D H V X
16	448.6 (+2)	E Z A H S X V X
16	448.9 (+2)	Y H H D X V X
16	454.3 (+2)	M A G A W C R X
16	456.7 (+2)	S H <u>D</u> <u>G</u> <u>S</u> V P T X
16	464.2 (+2)	F H - - X X X

TABLE D CONT'D.

16	469.9 (+2)	E H - - - T V X
16	472.3 (+2)	M A X - - - V V
16	499.0 (+2)	G H A <u>X</u> T D G X T X
16	504.1 (+2)	P V <u>S</u> H <u>X</u> V N E L
16	507.7 (+2)	X X Y T <u>P</u> <u>G</u> H T X
16	522.7 (+2)	- - - - - P V X
16	523.3 (+2)	M A H S - - P V F
16	529.9 (+2)	X H Y D R N Q X
16	536.2 (+2)	E A - - C Z V T T Y
16	547.9 (+2)	- - - - - A X S V
16	552.4 (+2)	X Z <u>A</u> <u>P</u> T S V F Z X
17	367.7 (+3)	<u>E</u> T M <u>P</u> A H P S T X
17	490.8 (+2)	M T X G Y G E P X
17	557.3 (+2)	A H G R K M S K S L
17	340.7 (+3)	- <u>H</u> - - H A Z V X
17	367.7 (+3)	- - - - R X S H X
17	419.8 (+2)	- - - H A V G X X
17	462.8 (+2)	M S S N E X X M
17	476.2 (+2)	G H - - - P C C
17	504.2 (+2)	X H V X A V N E X
17	523.2 (+2)	- H - - - - P V F
17	543.2 (+2)	X H E V Z P H X X
17	590.2 (+2)	A T E H <u>C</u> <u>E</u> V M E X
18	456.4 (+2)	A H S N L A S V L
18	463.3 (+2)	V X A P A N D X X
18	474.8 (+2)	M X <u>G</u> <u>X</u> S F P A X
18	491.2 (+2)	V H T C V N P V X
18	497.8 (+2)	S H Q R Q L L L
18	515.8 (+2)	E W <u>H</u> <u>Y</u> P V S X
18	519.7 (+2)	<u>F</u> H M <u>D</u> X Z T F
18	543.4 (+2)	X H E <u>V</u> <u>Z</u> P H X X
18	596.8 (+2)	<u>F</u> <u>H</u> <u>H</u> T Z S N P X X
19	434.6 (+2)	- H <u>G</u> <u>C</u> <u>P</u> G M P X
19	496.6 (+2)	<u>E</u> T <u>P</u> <u>E</u> H A P V X
19	539.6 (+2)	<u>M</u> <u>X</u> P G N S A X Y X

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

TABLE E

fraction	ion for MS/MS	derived peptide sequence
7	504.1 (+2)	H M S G Z P T S Y
7	549.2 (+2)	H N Z A A H Z E Y
8	517.0 (+2)	N Q Z H G S A E Y
8	526.0 (+2)	H A A <u>X</u> <u>Y</u> <u>S</u> Z V Y
8	642.7 (+2)	P M N D W X M T Z T Y
10	465.3 (+2)	S Q F G G G S Q Y
10	484.3 (+2)	Y Q S <u>D</u> <u>H</u> R Y
10	509.0 (+2)	F L Z A M Z S T Y
10	532.0 (+2)	T V X D S Z T H Y
11	424.3 (+2)	H X S T Z D F
11	464.3 (+2)	H A P P T D P P P
11	550.0 (+2)	H G P A N <u>R</u> <u>D</u> <u>S</u> V F
11	563.3 (+2)	F P Y P T D P Z Y
12	531.2 (+2)	K N A N L V Q L Y
14	585.6 (+2)	R S F X X E N E Y
16	488.7 (+2)	H M Z N P T S Y
16	661.9 (+2)	Y V X F - - - V Y
17	577.6 (+2)	R S M X <u>R</u> <u>C</u> <u>P</u> E Y
18	451.1 (+2)	I L G P P G S V Y
18	523.0 (+2)	- - <u>F</u> <u>V</u> T A Z T Y
19	565.6 (+2)	Y M I D P S G V S Y
19	503.8 (+2)	S Q X A A G V D V F
20	560.0 (+2)	X V E X T T D Y Y
20	582.4 (+2)	M Y N <u>C</u> <u>N</u> E X D Y
21	448.2 (+2)	A A G X G P T F Y
21	614.0 (+2)	I A V G Y V D D T Q F
22	507.2 (+2)	V A <u>F</u> <u>V</u> <u>X</u> F V G Y
22	557.2 (+2)	Y N <u>R</u> <u>W</u> S X E F
23	510.8 (+2)	<u>A</u> <u>L</u> M P - - X N Y
25	562.8 (+2)	N Q F Q A L L Q Y

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.